

# BLAST Basic Local Alignment Search Tool

Job Title: X70683:H.sapiens mRNA for SOX-4 protein

Please, try our new design!

BLASTN 2.2.18+

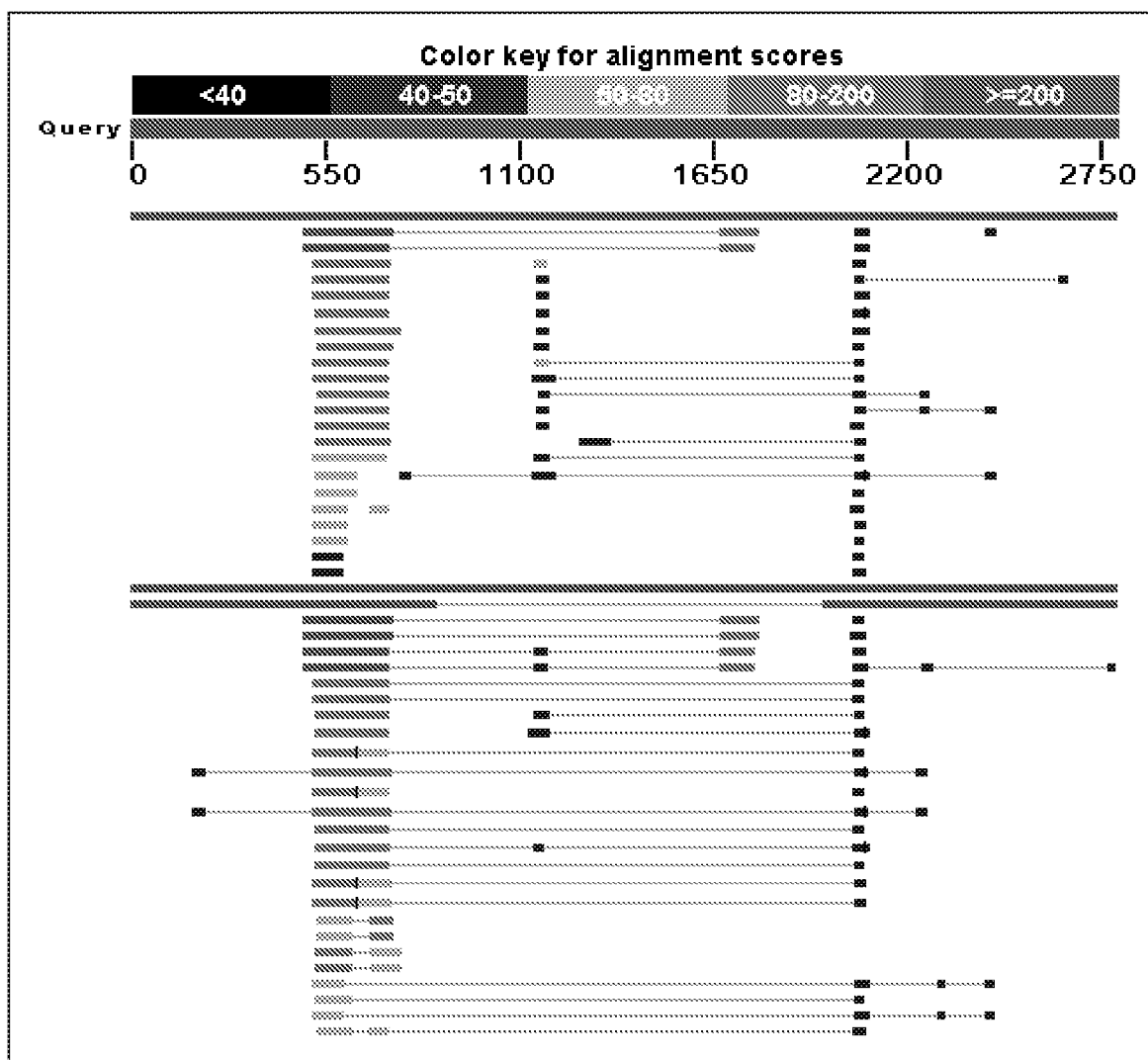
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 7WFMZ732012 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

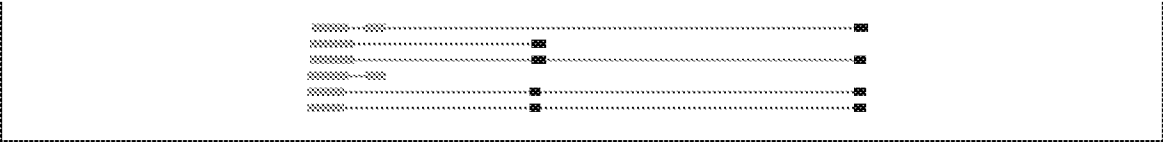
Genome View






Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= gi|36552|emb|X70683.1|HSSOX4M H.sapiens mRNA for SOX-4 protein Length=2797















































## Distribution of 270 Blast Hits on the Query Sequence










Distance tree of results [NEW](#)Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map ViewerSequences producing significant alignments:  
(Click headers to sort columns)

## Transcripts

NM_003107.2	Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA	5012	5012	99%	0.0	99%	 
NM_003108.3	Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA	309	440	13%	1e-80	86%	 
NM_006943.2	Homo sapiens SRY (sex determining region Y)-box 12 (SOX12), mRNA	291	422	12%	3e-75	88%	 
NM_006941.3	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA	167	167	7%	7e-38	77%	 
NM_000346.2	Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA	156	156	7%	1e-34	75%	
NM_007084.2	Homo sapiens SRY (sex determining region Y)-box 21 (SOX21), mRNA	140	140	7%	1e-29	74%	 
NM_006942.1	Homo sapiens SRY (sex determining region Y)-box 15 (SOX15), mRNA	129	129	7%	2e-26	74%	 
NM_014587.2	Homo sapiens SRY (sex determining region Y)-box 8 (SOX8), mRNA	127	127	8%	7e-26	71%	 
NM_031439.2	Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA	113	113	7%	1e-21	71%	 
NM_018419.2	Homo sapiens SRY (sex determining region Y)-box 18 (SOX18), mRNA	107	107	7%	6e-20	71%	 
NM_004189.2	Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA	104	104	7%	8e-19	71%	 
NM_022454.3	Homo sapiens SRY (sex determining region Y)-box 17 (SOX17), mRNA	100	100	7%	9e-18	71%	 
NM_005634.2	Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA	100	100	7%	9e-18	71%	 
NM_005986.2	Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA	96.9	96.9	7%	1e-16	70%	 
NM_003106.2	Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA	91.5	91.5	7%	5e-15	69%	 
NM_005686.2	Homo sapiens SRY (sex determining region Y)-box 13 (SOX13), mRNA	78.8	78.8	7%	3e-11	70%	 
XM_001713691.1	PREDICTED: Homo sapiens hypothetical protein LOC100130809 (LOC100130809), mRNA	64.4	64.4	4%	7e-07	74%	
NM_003140.1	Homo sapiens sex determining region Y (SRY), mRNA	64.4	64.4	4%	7e-07	74%	 
NM_152989.2	Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA	57.2	57.2	3%	1e-04	73%	 
NM_006940.4	Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 1, mRNA	57.2	57.2	3%	1e-04	73%	 
NM_178010.1	Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 3, mRNA	57.2	57.2	3%	1e-04	73%	 
NM_052876.2	Homo sapiens BTB (POZ) domain containing 14B (BTBD14B), mRNA	51.8	51.8	1%	0.004	89%	 
NM_033326.2	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), transcript variant 2, mRNA	50.0	50.0	3%	0.014	72%	 
NM_017508.1	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), transcript variant 1, mRNA	50.0	50.0	3%	0.014	72%	 

XM_001132155.2	PREDICTED: Homo sapiens similar to Afadin (Protein AF-6) (LOC730031), mRNA	46.4	46.4	1%	0.18	88%	
NM_001040001.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 1, mRNA	46.4	46.4	1%	0.18	88%	
NM_001040000.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 2, mRNA	46.4	46.4	1%	0.18	88%	
NM_005936.2	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 3, mRNA	46.4	46.4	1%	0.18	88%	
NM_015156.2	Homo sapiens REST corepressor 1 (RCOR1), mRNA	44.6	44.6	1%	0.62	83%	

## Genomic sequences [show first]


NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	5012	5094	99%	0.0	99%
NW_001838973.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188126)	1570	3057	60%	0.0	100%
NW_001838765.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188139)	309	440	13%	1e-80	86%
NT_005334.15	Homo sapiens chromosome 2 genomic contig, reference assembly	309	440	13%	1e-80	86%
NW_001838652.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188366)	291	601	13%	3e-75	88%
NT_011387.8	Homo sapiens chromosome 20 genomic contig, reference assembly	291	601	13%	3e-75	88%
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	140	182	8%	1e-29	90%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	140	182	8%	1e-29	90%
NW_001838403.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188371)	129	129	7%	2e-26	74%
NT_010718.15	Homo sapiens chromosome 17 genomic contig, reference assembly	129	129	7%	2e-26	74%
NW_001838454.2	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188168)	104	246	8%	8e-19	90%
NW_001838884.2	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188385)	104	366	11%	8e-19	92%
NT_010641.15	Homo sapiens chromosome 17 genomic contig, reference assembly	104	163	7%	8e-19	78%
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	104	448	11%	8e-19	92%
NW_001842405.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188404)	100	141	8%	9e-18	87%
NT_011786.15	Homo sapiens chromosome X genomic contig, reference assembly	100	223	10%	9e-18	92%
NT_027140.6	Homo sapiens chromosome 13 genomic contig, reference assembly	96.9	137	8%	1e-16	92%
NW_001838745.1	Homo sapiens chromosome 22 genomic contig,	95.1	255	9%	4e-16	96%

	alternate assembly (based on HuRef SCAF_1103279188372)					
NT_011520.11	Homo sapiens chromosome 22 genomic contig, reference assembly	95.1	255	9%	4e-16	96%
NW_001839122.2	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188150)	87.8	141	6%	6e-14	87%
NT_077531.3	Homo sapiens chromosome 8 genomic contig, reference assembly	87.8	141	6%	6e-14	87%
NW_001838339.2	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279188181)	86.0	139	7%	2e-13	77%
NT_037887.4	Homo sapiens chromosome 16 genomic contig, reference assembly	86.0	139	7%	2e-13	77%
NW_001838533.2	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188157)	77.0	335	6%	1e-10	100%
NW_001838085.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188104)	77.0	117	4%	1e-10	92%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	77.0	376	6%	1e-10	100%
NW_001839132.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188282)	66.2	285	7%	2e-07	92%
NT_008183.18	Homo sapiens chromosome 8 genomic contig, reference assembly	66.2	328	7%	2e-07	92%
NW_001842422.1	Homo sapiens chromosome Y genomic contig, alternate assembly (based on HuRef SCAF_1103279188414)	64.4	108	5%	7e-07	84%
NT_011896.9	Homo sapiens chromosome Y genomic contig, reference assembly	64.4	192	7%	7e-07	87%
NT_011333.5	Homo sapiens chromosome 20 genomic contig, reference assembly	62.6	116	6%	2e-06	79%
NW_001838052.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188408)	57.2	140	5%	1e-04	96%
NT_009714.16	Homo sapiens chromosome 12 genomic contig, reference assembly	57.2	181	5%	1e-04	96%
NW_001838671.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188118)	53.6	53.6	2%	0.001	79%
NW_001838954.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188298)	51.8	180	5%	0.004	90%
NT_011295.10	Homo sapiens chromosome 19 genomic contig, reference assembly	51.8	92.7	2%	0.004	96%
NT_023133.12	Homo sapiens chromosome 5 genomic contig, reference assembly	51.8	180	5%	0.004	90%
NW_001838022.2	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279188392)	50.0	131	5%	0.014	92%
NW_001838468.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188038)	50.0	50.0	1%	0.014	87%
NW_001838951.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188395)	50.0	94.5	1%	0.014	87%
NW_001838865.2	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188138)	50.0	50.0	1%	0.014	87%

NT_006576.15	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0	131	2%	0.014	100%
NT_009237.17	Homo sapiens chromosome 11 genomic contig, reference assembly	50.0	131	5%	0.014	92%
NT_007819.16	Homo sapiens chromosome 7 genomic contig, reference assembly	50.0	347	6%	0.014	96%
NT_010966.13	Homo sapiens chromosome 18 genomic contig, reference assembly	50.0	50.0	1%	0.014	87%
NT_010393.15	Homo sapiens chromosome 16 genomic contig, reference assembly	50.0	131	3%	0.014	92%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	50.0	176	3%	0.014	100%
NT_006713.14	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0	135	1%	0.014	88%
NW_001838061.2	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188362)	46.4	251	1%	0.18	92%
NW_001838006.2	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on HuRef SCAF_1103279188397)	46.4	130	1%	0.18	93%
NW_001838988.2	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279187031)	46.4	46.4	1%	0.18	93%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	210	3%	0.18	93%
NT_113898.1	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	46.4	1%	0.18	88%
NT_007302.13	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	46.4	1%	0.18	88%
NT_030059.12	Homo sapiens chromosome 10 genomic contig, reference assembly	46.4	171	1%	0.18	93%
NW_001838769.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188433)	44.6	210	4%	0.62	96%
NW_001838115.2	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on HuRef SCAF_1103279188327)	44.6	85.5	2%	0.62	96%
NW_001838461.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188344)	44.6	44.6	1%	0.62	90%
NW_001838768.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188306)	44.6	44.6	1%	0.62	83%
NW_001838987.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188274B)	44.6	85.5	1%	0.62	92%
NW_001838928.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188369)	44.6	44.6	0%	0.62	96%
NW_001838915.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on HuRef SCAF_1103279188399)	44.6	249	1%	0.62	96%
NW_001838878.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188187)	44.6	85.5	1%	0.62	90%
NW_001838953.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188146)	44.6	44.6	1%	0.62	88%
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	44.6	249	2%	0.62	92%
NT_016354.18		44.6	536	1%	0.62	96%

	Homo sapiens chromosome 4 genomic contig, reference assembly					
NT_023935.17	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	130	3%	0.62	92%
NT_008470.18	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	169	4%	0.62	93%
NT_022459.14	Homo sapiens chromosome 3 genomic contig, reference assembly	44.6	85.5	1%	0.62	90%
NT_032977.8	Homo sapiens chromosome 1 genomic contig, reference assembly	44.6	374	3%	0.62	96%
NT_010859.14	Homo sapiens chromosome 18 genomic contig, reference assembly	44.6	44.6	1%	0.62	90%

## Alignments

>ref|NM\_003107.2|  Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA  
Length=4912

GENE ID: 6659 SOX4 | SRY (sex determining region Y)-box 4 [Homo sapiens]  
(Over 10 PubMed links)


Score = 5012 bits (5558), Expect = 0.0  
Identities = 2789/2793 (99%), Gaps = 2/2793 (0%)  
Strand=Plus/Plus

Query	5	CCAGCATTTCGAGAAACTCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAGACAG	64
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```
Sbjct  2609  GTCTGCACCCCCAGCAAGAAGGCGAGTTAGTTTTCTAGAGACTTGAAGGAGTCTCCCCCT  2668
Query  2223  TCCTGCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGGTCAAGAAAGGAGGGGAGA  2282
          |||
Sbjct  2669  TCCTGCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGGTCAAGAAAGGAGGGGAGA  2728
Query  2283  ACCCAGCGCACCCCTTGGGCGGCTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGG  2342
          |||
Sbjct  2729  ACCCAGCGCACCCCTCCCCCCTTTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGG  2788
Query  2343  TGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC  2402
          |||
Sbjct  2789  TGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC  2848
Query  2403  AGGCGAATTCCCGTTTGGGGCCTTTTCTCCCTCTTTTCCCTTGCCCCCTCTGCAG  2462
          |||
Sbjct  2849  AGGCGAATTCCCGTTTGGGGCTTTTTTCTCCCTCTTTTCCCTTGCCCCCTCTGCAG  2908
Query  2463  CCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC  2522
          |||
Sbjct  2909  CCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC  2968
Query  2523  CCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGGACACG  2582
          |||
Sbjct  2969  CCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGGACACG  3028
Query  2583  AACTGGAAGGGGGTTACGGTCAAAC TGAAATGGATTTGCACGTTGGGGAGCTGGCGGCG  2642
          |||
Sbjct  3029  AACTGGAAGGGGGTTACGGTCAAAC TGAAATGGATTTGCACGTTGGGGAGCTGGCGGCG  3088
Query  2643  GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA  2702
          |||
Sbjct  3089  GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA  3148
Query  2703  CCCCAGGAGCGTGAGGAGAGGAGACTGTTTGATGTGGTACAGGGGCAGTCAGTGGAGGG  2762
          |||
Sbjct  3149  CCCCAGGAGCGTGAGGAGAGGAGACTGTTTGATGTGGTACAGGGGCAGTCAGTGGAGGG  3208
Query  2763  CGAGTGGTTTTCGGAAAAAAAAAG  2795
          |||
Sbjct  3209  CGAGTGGTTTTCGGAAAAAAAAAG  3241
```

>ref|NM\_003108.3|  Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA  
Length=8737

GENE ID: 6664 SOX11 | SRY (sex determining region Y)-box 11 [Homo sapiens]  
(Over 10 PubMed links)

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Score = 309 bits (342), Expect = 1e-80  
Identities = 224/259 (86%), Gaps = 0/259 (0%)  
Strand=Plus/Plus


```
Query  491  CGACCCGAGCTGGTGAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCAT  550
          |||
Sbjct  166  CGACCCAGACTGGTGAAGACGGCGTCGGGCCACATCAAGCGGCCGATGAACGCCTTCAT  225
Query  551  GGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCAGATGCACAACGC  610
          |||
Sbjct  226  GGTATGGTCCAAGATCGAACGCAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC  285
Query  611  CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC  670
          |||
Sbjct  286  CGAGATCTCCAAGAGGCTGGGCAAACGCTGGAAGCTGCTGAAGGACAGCGAGAAGATCCC  345
Query  671  TTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAA  730
          |||
Sbjct  346  GTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCCGACTACCCCGACTACAA  405
Query  731  GTACCGGCCCAGGAAGAAG  749
          |||
Sbjct  406  GTACCGGCCCCGAAAAAG  424
```

Score = 131 bits (144), Expect = 5e-27  
Identities = 96/112 (85%), Gaps = 0/112 (0%)

Strand=Plus/Plus

```
Query 1671 GGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGA 1730
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1277 GGCTCCCCTTCGAGTTCCCCGACTACTGCACGCCCGAGCTGAGCGAGATGATCGCGGG 1336

Query 1731 GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTACCTACTGAAGGGCGC 1782
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1337 GACTGGCTGGAGGCGAACTTCTCCGACCTGGTGTTCACATATTGAAAGGCGC 1388
```

>ref|NM\_006943.2|  Homo sapiens SRY (sex determining region Y)-box 12 (SOX12), mRNA  
Length=4645

GENE ID: 6666 SOX12 | SRY (sex determining region Y)-box 12 [Homo sapiens]  
(10 or fewer PubMed links)

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Score = 291 bits (322), Expect = 3e-75  
Identities = 213/246 (86%), Gaps = 1/246 (0%)  
Strand=Plus/Plus

```
Query 494 CCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT 553
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 418 CCCG-GCTGGTGCAAGACCCCGAGCGGCCACATCAAGAGGCCGATGAACGCATTTCATGGT 476

Query 554 GTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACATGCACAACGCCGA 613
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 477 GTGGTCGCAGCACGAACGGCGGAAGATCATGGACCACTGGCCCCGACATGCACAACGCCGA 536

Query 614 GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT 673
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 537 GATCTCCAAGCGCCTGGGCCGCCGCTGGCAGCTGCTGCAGGACTCGGAGAAGATCCCGTT 596


Query 674 CATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA 733
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 597 CGTGCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA 656

Query 734 CCGGCC 739
          |||||
Sbjct 657 CCGGCC 662
```

Score = 131 bits (144), Expect = 5e-27  
Identities = 90/102 (88%), Gaps = 0/102 (0%)  
Strand=Plus/Plus

```
Query 1674 TCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1177 TCGCACTTCGAGTTCCCGGACTACTGCACCCCGAGGTTACCGAGATGATCGCGGGGGAC 1236

Query 1734 TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTACCTACTGA 1775
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1237 TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTTACCTACTGA 1278
```

>ref|NM\_006941.3|  Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA  
Length=2882

GENE ID: 6663 SOX10 | SRY (sex determining region Y)-box 10 [Homo sapiens]  
(Over 10 PubMed links)

Score = 167 bits (184), Expect = 7e-38  
Identities = 173/224 (77%), Gaps = 2/224 (0%)  
Strand=Plus/Plus


```
Query 521 GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTTCGAGATCGAGCGGCGCAAGAT 580
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 584 GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT 643

Query 581 CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG 640
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 644 CGCGGACCACTACCCGCACCTGCACAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG 703

Query 641 GAAGCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCC 699
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```




```
Sbjct 701 GCAGAACCCCCAAGATGCACAACCTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGGAAGCT 760
Query 647 GCTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA 706
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 761 GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCCGACA 820
Query 707 CATGGCTGACTACCCCGACTACAAGTACCGGCC 739
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 821 CCTGCGCGACTACCCCGACTACAAGTACCGGCC 853
```

>ref|NM\_014587.2|  Homo sapiens SRY (sex determining region Y)-box 8 (SOX8), mRNA  
Length=3069

GENE ID: 30812 SOX8 | SRY (sex determining region Y)-box 8 [Homo sapiens]  
(Over 10 PubMed links)

Score = 127 bits (140), Expect = 7e-26  
Identities = 179/252 (71%), Gaps = 6/252 (2%)  
Strand=Plus/Plus


```
Query 528 AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG 587
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 422 AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGGCGCGCCGCAAGCTGGCCGAC 481
Query 588 CAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTG 647
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 482 CAGTACCCGACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTGTGGCGCTTG 541
Query 648 CTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCAC 707
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 542 CTGAGCGGAGAGCGAGAAGCGGCCCTTCGTGGAGGAGGCAGAGCGCCTTCGCGTGCAGCAC 601
Query 708 ATGGCTGACTACCCCGACTACAAGTAC-----CGGCCAGGAAGAAGGTGAAGTCCGGC 761
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 602 AAGAAGGACCACCCCGACTACAAGTACCAGCCACGGCGCAGGAAGAGCGCCAAAGCCGGC 661
Query 762 AACGCCAACTCC 773
      ||| ||| ||| |||
Sbjct 662 CACAGCGACTCC 673
```

>ref|NM\_031439.2|  Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA  
Length=3219

GENE ID: 83595 SOX7 | SRY (sex determining region Y)-box 7 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 113 bits (124), Expect = 1e-21  
Identities = 159/223 (71%), Gaps = 3/223 (1%)  
Strand=Plus/Plus

```
Query 530 GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCA 589
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 217 GCGGCCCATGAACGCCTTCATGGTTTGGGCCAAGGACGAGAGGAAACGGCTGGCAGTGCA 276
Query 590 GTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCT 649
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 277 GAACCCGGACCTGCACAACGCCGAGCTCAGCAAGATGCTGGGAAAGTCGTGGAAGGCGCT 336
Query 650 CAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACAT 709
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 337 GACGCTGTCCCAGAAGAGGCCGTACGTGGACGAGGCGGAGCGGCTGCGCCTGCAGCACAT 396
Query 710 GGCTGACTACCCCGACTACAAGTACCGGCC---CAGGAAGAAG 749
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 397 GCAGGACTACCCCAACTACAAGTACCGGCCGCGCAGGAAGAAG 439
```

>ref|NM\_018419.2|  Homo sapiens SRY (sex determining region Y)-box 18 (SOX18), mRNA  
Length=1718

GENE ID: 54345 SOX18 | SRY (sex determining region Y)-box 18 [Homo sapiens]  
(Over 10 PubMed links)

Score = 107 bits (118), Expect = 6e-20  
Identities = 160/223 (71%), Gaps = 8/223 (3%)  
Strand=Plus/Plus

7/16/08



(Over 10 PubMed links)


Score = 78.8 bits (86), Expect = 3e-11  
Identities = 153/218 (70%), Gaps = 10/218 (4%)  
Strand=Plus/Plus

```
Query  522  CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC  581
          |||||
Sbjct  1862  CACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATC  1921

Query  582  ATG-GAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG  640
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct  1922  CTGCAAGCCTTC-CCAGACATGCACAACCTCCAGCATCAGCAAGATCCTTGGATCTCGCTG  1980

Query  641  GAAG---CTGCTCAAAGACAGCGACAAG-ATCCCTTTTCATTCGAGAGGCGGAGCGGCTGC  696
          ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct  1981  GAAGTCCATGACCAA--CCAG-GAGAAGCAGCCCTACTATGAG-GAACAGGCGCGGCTGA  2036

Query  697  GCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC  734
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct  2037  GCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTAC  2074
```


>ref|XM\_001713691.1|  PREDICTED: Homo sapiens hypothetical protein LOC100130809 (LOC10013 mRNA)  
Length=897

Score = 64.4 bits (70), Expect = 7e-07  
Identities = 94/126 (74%), Gaps = 8/126 (6%)  
Strand=Plus/Plus

```
Query  528  AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT  583
          |||||
Sbjct  329  AAGCGACCCATGAACGCATTTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT  387

Query  584  GGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA  643
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct  388  AGAG-AATC-CCAGA-ATGCGAAACTCAGAGATCAGCAAGCAGCTGGGATACCAGTGGAA  444

Query  644  GCTGCT  649
          ||||
Sbjct  445  AATGCT  450
```

>ref|NM\_003140.1|  Homo sapiens sex determining region Y (SRY), mRNA  
Length=897


GENE ID: 6736 SRY | sex determining region Y [Homo sapiens]  
(Over 10 PubMed links)

Score = 64.4 bits (70), Expect = 7e-07  
Identities = 94/126 (74%), Gaps = 8/126 (6%)  
Strand=Plus/Plus

```
Query  528  AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT  583
          |||||
Sbjct  329  AAGCGACCCATGAACGCATTTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT  387

Query  584  GGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA  643
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct  388  AGAG-AATC-CCAGA-ATGCGAAACTCAGAGATCAGCAAGCAGCTGGGATACCAGTGGAA  444

Query  644  GCTGCT  649
          ||||
Sbjct  445  AATGCT  450
```

>ref|NM\_152989.2|  Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcribed variant 2, mRNA  
Length=4563


GENE ID: 6660 SOX5 | SRY (sex determining region Y)-box 5 [Homo sapiens]  
(Over 10 PubMed links)

Score = 57.2 bits (62), Expect = 1e-04  
Identities = 76/103 (73%), Gaps = 2/103 (1%)  
Strand=Plus/Plus



```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT 580
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1995 CACATAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT 2053

Query 581 CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG 623
          || | | | | | | | | | | | | | | | | | | | | | |
Sbjct 2054 CCTTCAAGCCTTTCTGACATGCACAACCTCCAACATCAGCAAG 2096
```


>ref|NM\_006940.4|  Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcribed variant 1, mRNA  
Length=4333

GENE ID: 6660 SOX5 | SRY (sex determining region Y)-box 5 [Homo sapiens]  
(Over 10 PubMed links)

Score = 57.2 bits (62), Expect = 1e-04  
Identities = 76/103 (73%), Gaps = 2/103 (1%)  
Strand=Plus/Plus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT 580
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1765 CACATAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT 1823

Query 581 CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG 623
          || | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1824 CCTTCAAGCCTTTCTGACATGCACAACCTCCAACATCAGCAAG 1866
```


>ref|NM\_178010.1|  Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcribed variant 3, mRNA  
Length=3095

GENE ID: 6660 SOX5 | SRY (sex determining region Y)-box 5 [Homo sapiens]  
(Over 10 PubMed links)

Score = 57.2 bits (62), Expect = 1e-04  
Identities = 76/103 (73%), Gaps = 2/103 (1%)  
Strand=Plus/Plus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT 580
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 527 CACATAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT 585


Query 581 CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG 623
          || | | | | | | | | | | | | | | | | | | | | | |
Sbjct 586 CCTTCAAGCCTTTCTGACATGCACAACCTCCAACATCAGCAAG 628
```

>ref|NM\_052876.2|  Homo sapiens BTB (POZ) domain containing 14B (BTBD14B), mRNA  
Length=4556

GENE ID: 112939 BTBD14B | BTB (POZ) domain containing 14B [Homo sapiens]  
(10 or fewer PubMed links)

Score = 51.8 bits (56), Expect = 0.004  
Identities = 34/38 (89%), Gaps = 0/38 (0%)  
Strand=Plus/Minus

```
Query 1149 GCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 67 GCCTCGGCCTCCGCCTCCGCGGCCTCCGCGGCCTCCGC 30
```

>ref|NM\_033326.2|  Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), transcribed variant 2, mRNA  
Length=5048

GENE ID: 55553 SOX6 | SRY (sex determining region Y)-box 6 [Homo sapiens]  
(Over 10 PubMed links)

Score = 50.0 bits (54), Expect = 0.014  
Identities = 65/90 (72%), Gaps = 0/90 (0%)  
Strand=Plus/Plus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC 581
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1859 CACATTAAGCGACCAATGAATGCATTTCATGGTTTGGGCAAAGGATGAGAGGAGAAAAATC 1918

Query 582 ATGGAGCAGTCGCCCCGACATGCACAACGCC 611
| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1919 CTTCAGGCCTTCCCCGACATGCATAACTCC 1948
```

>ref|NM\_017508.1| **UGM** Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), transcript variant 1, mRNA  
Length=5158

GENE ID: 55553 SOX6 | SRY (sex determining region Y)-box 6 [Homo sapiens]  
(Over 10 PubMed links)

Score = 50.0 bits (54), Expect = 0.014  
Identities = 65/90 (72%), Gaps = 0/90 (0%)  
Strand=Plus/Plus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC 581
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1969 CACATTAAGCGACCAATGAATGCATTTCATGGTTTGGGCAAAGGATGAGAGGAGAAAAATC 2028

Query 582 ATGGAGCAGTCGCCCCGACATGCACAACGCC 611
| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 2029 CTTCAGGCCTTCCCCGACATGCATAACTCC 2058
```

>ref|XM\_001132155.2| **GM** PREDICTED: Homo sapiens similar to Afadin (Protein AF-6) (LOC730031 mRNA  
Length=1522

Score = 46.4 bits (50), Expect = 0.18  
Identities = 31/35 (88%), Gaps = 0/35 (0%)  
Strand=Plus/Minus

```
Query 1155 GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 107 GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC 73
```

>ref|NM\_001040001.1| **UGM** Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritho homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 1, mRNA  
Length=7762

GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Homo sapiens] (Over 10 PubMed links)

Score = 46.4 bits (50), Expect = 0.18  
Identities = 31/35 (88%), Gaps = 0/35 (0%)  
Strand=Plus/Minus


```
Query 1155 GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 38 GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC 4
```

>ref|NM\_001040000.1| **UGM** Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritho homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 2, mRNA  
Length=7551

GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Homo sapiens] (Over 10 PubMed links)

Score = 46.4 bits (50), Expect = 0.18  
Identities = 31/35 (88%), Gaps = 0/35 (0%)  
Strand=Plus/Minus


```
Query 1155 GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 38 GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC 4
```

>ref|NM\_005936.2|  Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 3, mRNA  
Length=4981

GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Homo sapiens] (Over 10 PubMed links)

Score = 46.4 bits (50), Expect = 0.18  
Identities = 31/35 (88%), Gaps = 0/35 (0%)  
Strand=Plus/Minus


Query	1155	GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC	1189
Sbjct	38	GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC	4

>ref|NM\_015156.2|  Homo sapiens REST corepressor 1 (RCOR1), mRNA  
Length=5537

GENE ID: 23186 RCOR1 | REST corepressor 1 [Homo sapiens] (Over 10 PubMed links)

Score = 44.6 bits (48), Expect = 0.62  
Identities = 35/42 (83%), Gaps = 0/42 (0%)  
Strand=Plus/Plus

Query	1148	CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC	1189
Sbjct	126	CGCCTCGGGCGCCGCCGCTCCTCAGCCTCGGCCGCCGCCGC	167

>ref|NT\_007592.14|Hs6\_7749  Homo sapiens chromosome 6 genomic contig, reference assembly  
Length=48945890

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 4

Score = 5012 bits (5558), Expect = 0.0  
Identities = 2789/2793 (99%), Gaps = 2/2793 (0%)  
Strand=Plus/Plus

Query	5	CCAGCATTTCGAGAACTCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAGACAG	64
Sbjct	12452671	CCAGCATTTCGAGAACTCCTCTCTACTTTAGCACGGTCTCCAGACTCAGCCGAGAGACAG	12452730
Query	65	CAAAGTGGGCGGGTGGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCCTGGGAA	124
Sbjct	12452731	CAAAGTGCAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCCTGGGAA	12452790
Query	125	CTATAACTCCTCTGCGAGAGGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	184
Sbjct	12452791	CTATAACTCCTCTGCGAGAGGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	12452850
Query	185	TCTTTACCCACCTCCGCCCCCTGCGAGGAGTTGAGGGGCCAGTTCGGCCGCCGCGCGCGTC	244
Sbjct	12452851	TCTTTACCCACCTCCGCCCCCTGCGAGGAGTTGAGGGGCCAGTTCGGCCGCCGCGCGCGTC	12452910
Query	245	TTCCCGTTTCGGCGTGTGCTTGGCCCCGGGGAACCGGGAGGGCCCCGGCGATCGCGCGGCGGC	304
Sbjct	12452911	TTCCCGTTTCGGCGTGTGCTTGGCCCCGGGGAACCGGGAGGGCCCCGGCGATCGCGCGGCGGC	12452970
Query	305	CGCCGCGAGGGTGTGAGCGCGCGTGGGCGCCCGCCGAGCCGAGGCCATGGTGCAGCAAAC	364
Sbjct	12452971	CGCCGCGAGGGTGTGAGCGCGCGTGGGCGCCCGCCGAGCCGAGGCCATGGTGCAGCAAAC	12453030
Query	365	CAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGCGAGAGCTCGGACTCGGGCGCCGG	424
Sbjct	12453031	CAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGCGAGAGCTCGGACTCGGGCGCCGG	12453090
Query	425	CCTCGAGCTGGGAATCGCCTCCTCCCCACGCCCCGGCTCCACCGCCTCCACGGGCGGCAA	484
Sbjct	12453091	CCTCGAGCTGGGAATCGCCTCCTCCCCACGCCCCGGCTCCACCGCCTCCACGGGCGGCAA	12453150
Query	485	GGCCGACGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGC	544

Sbjct	12453151	GGCCGACGACCCGAGCTGGTGCAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGC	12453210
Query	545	CTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACATGCA	604
Sbjct	12453211	CTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACATGCA	12453270
Query	605	CAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAA	664
Sbjct	12453271	CAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAA	12453330
Query	665	GATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGA	724
Sbjct	12453331	GATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGA	12453390
Query	725	CTACAAGTACCGGCCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	784
Sbjct	12453391	CTACAAGTACCGGCCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	12453450
Query	785	CGCCGCCTCCTCCAAGCCGGGGGAGaagggagacaaggtcggtagtggcggggggcgg	844
Sbjct	12453451	CGCCGCCTCCTCCAAGCCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGCGGGGGCGG	12453510
Query	845	ccatggggggcggcgggcgggcgggagcagcaacgcggggggaggaggcggtcgagag	904
Sbjct	12453511	CCATGGGGGCGGCGGCGGCGGGGAGCAGCAACGCGGGGGGAGGAGGCGGCGGTGCGAG	12453570
Query	905	tggcgggcgggcgaactccaaaccggcgcgagaaaaagagctgCGGCTCCAAAGTGGCGGG	964
Sbjct	12453571	TGGCGGCGGCGCCAACCTCCAAACCGGCGCAGAAAAAGAGCTGCGGCTCCAAAGTGGCGGG	12453630
Query	965	CGGCGCGGGCGGTGGGGTTAGCAAACCGCACGCCAAGCTCATCTTGGCaggcgggcgggcg	1024
Sbjct	12453631	CGGCGCGGGCGGTGGGGTTAGCAAACCGCACGCCAAGCTCATCTTGGCAGGCGGCGGCGG	12453690
Query	1025	cggcggaagagcagcggttgccgccgccgcctccttcgccgccgaacaggcgggggccgc	1084
Sbjct	12453691	CGGCGGGAAAGCAGCGGCTGCCGCCGCCGCCTCCTTCGCCGCCGAACAGGCGGGGGCCGC	12453750
Query	1085	cgccctgctgcccctgggCGCCGCCGCCGACCACCCTCGCTGTACAAGGCGCGGACTCC	1144
Sbjct	12453751	CGCCCTGCTGCCCCTGGGCGCCGCCGCCGACCACCCTCGCTGTACAAGGCGCGGACTCC	12453810
Query	1145	CAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCCGGG	1204
Sbjct	12453811	CAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCCGGG	12453870
Query	1205	CAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTTCGGCGGCCTGGGCACGTC	1264
Sbjct	12453871	CAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTTCGGCGGCCTGGGCACGTC	12453930
Query	1265	GTCGTCGCCCCTGGGCGGCGTGGGCGCGGGAGCCGACCCAGCGACCCCCTGGGCCTGTA	1324
Sbjct	12453931	GTCGTCGCCCCTGGGCGGCGTGGGCGCGGGAGCCGACCCAGCGACCCCCTGGGCCTGTA	12453990
Query	1325	CGAGGAGGAGGGCGCGGGCTGCTcgcccgacgagcgccagcccgagcgggcgccgacgagc	1384
Sbjct	12453991	CGAGGAGGAGGGCGCGGGCTGCTCGCCCCGACGCGCCAGCCTGAGCGGCCGCAGCAGCGC	12454050
Query	1385	cgccctgctccccgccgccggccgctcgcccgccgaccaccgCGGCTACGCCAGCCTGCG	1444
Sbjct	12454051	CGCCCTGCTCCCCGCCGCCGGCCGCTCGCCCGCCGACCACCgCGGCTACGCCAGCCTGCG	12454110
Query	1445	cgcggcctcgcccgcccccgtccagcgcgccctcgCACGCGTcctcctcgccctcgtccca	1504
Sbjct	12454111	CGCCGCCTCGCCCGCCCCGTCCAGCGCGCCCTCGCACGCGTCTCCTCGGCCTCGTCCCA	12454170
Query	1505	ctcctcctctcttcctcctcctcctgggctcctcgtcctccgacgacagagttcgaaagacGACCT	1564
Sbjct	12454171	CTCCTCCTCTTCCTCCTCCTCGGGCTCCTCGTCCTCCGACGACGAGTTCGAAGACGACCT	12454230
Query	1565	GCTCGACCTGAACCCCAGCTCAAACCTTTGAGAGCATGTCCCTGGGCAGCTTCAGTTCGTC	1624
Sbjct	12454231	GCTCGACCTGAACCCCAGCTCAAACCTTTGAGAGCATGTCCCTGGGCAGCTTCAGTTCGTC	12454290
Query	1625	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA	1684
Sbjct	12454291	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA	12454350
Query	1685	GTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	1744
Sbjct	12454351	GTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	12454410

Query	1745	CAGCATCTCCAACCTGGTTTTTCACCTACTGAAGGGCGCGCAGGCAGGGAGAAGGGCCggg	1804
Sbjct	12454411	CAGCATCTCCAACCTGGTTTTTCACCTACTGAAGGGCGCGCAGGCAGGGAGAAGGGCCGGG	12454470
Query	1805	gggggTAGGAGAGGAGaaaaaaaagtgaaaaaaaagaaacgaaaaaggacagacgaagagt	1864
Sbjct	12454471	GGGGGTAGGAGAGGAGAAAAAAAAGTGAAAAAAGAAACGAAAAGGACAGACGAAGAGT	12454530
Query	1865	ttaaagagaaaagggaaaaaaggaagaaaaagtaagcaggggCTCG-TTCGCCCCGCTTCT	1923
Sbjct	12454531	TTAAAGAGAAAAGGGAAAAAAGAAAGAAAAAGTAAGCAGGGCTGGCTTCGCCCCGCTTCT	12454590
Query	1924	CGTCGTCGGATCAAGGAGCGCGGCGGCGTTTTGGACCCGCGCTCCCATCCCCACCTTCC	1983
Sbjct	12454591	CGTCGTCGGATCAAGGAGCGCGGCGGCGTTTTGGACCCGCGCTCCCATCCCCACCTTCC	12454650
Query	1984	CGGGCCGGGGACCCACTCTGCCCAGCCGGAGGGACGCGGAGGAGGAAGAGGGTAGACAGG	2043
Sbjct	12454651	CGGGCCGGGGACCCACTCTGCCCAGCCGGAGGGACGCGGAGGAGGAAGAGGGTAGACAGG	12454710
Query	2044	GGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGC-*****GCGACTT	2102
Sbjct	12454711	GGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAAAAAGCGACTT	12454770
Query	2103	CGAGTTTGCTCCCCCTTTGCTTGAAGAGACCCCTCCCCCTTCCAACGAGCTTCCGGACTT	2162
Sbjct	12454771	CGAGTTTGCTCCCCCTTTGCTTGAAGAGACCCCTCCCCCTTCCAACGAGCTTCCGGACTT	12454830
Query	2163	GTCTGCACCCCCAGCAAGAAGGCGAGTTAGTTTTCTAGAGACTTGAAGGAGTCTCCCCCT	2222
Sbjct	12454831	GTCTGCACCCCCAGCAAGAAGGCGAGTTAGTTTTCTAGAGACTTGAAGGAGTCTCCCCCT	12454890
Query	2223	TCCTGCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGGTCAAGAAAGGAGGGGAGA	2282
Sbjct	12454891	TCCTGCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGGTCAAGAAAGGAGGGGAGA	12454950
Query	2283	ACCCAGCGCACCCCTcccccccttttttAAACGCGTGATGAAGACAGAAGGCTCCGGGG	2342
Sbjct	12454951	ACCCAGCGCACCCCTCCCCCCTTTTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGG	12455010
Query	2343	TGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC	2402
Sbjct	12455011	TGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC	12455070
Query	2403	AGGCGAATTCCCGTTTGGGGCcttttttCCTCCCTCTTTTCCCCCTTGCCCCCTCTGCAG	2462
Sbjct	12455071	AGGCGAATTCCCGTTTGGGGCTTTTTTTTCTCCCTCTTTTCCCCCTTGCCCCCTCTGCAG	12455130
Query	2463	CCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC	2522
Sbjct	12455131	CCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC	12455190
Query	2523	CCGAGAACCCCGTTTGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGGACACG	2582
Sbjct	12455191	CCGAGAACCCCGTTTGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGGACACG	12455250
Query	2583	AACTGGAAGGGGGTTACGGTCAAACGAAATGGATTTGCACGTTGGGGAGCTGGCGGCG	2642
Sbjct	12455251	AACTGGAAGGGGGTTACGGTCAAACGAAATGGATTTGCACGTTGGGGAGCTGGCGGCG	12455310
Query	2643	GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA	2702
Sbjct	12455311	GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA	12455370
Query	2703	CCCCGGAGGCGTGGAGGAGAGGAGACTGTTTGATGTGGTACAGGGGCAGTCAGTGGAGGG	2762
Sbjct	12455371	CCCCGGAGGCGTGGAGGAGAGGAGACTGTTTGATGTGGTACAGGGGCAGTCAGTGGAGGG	12455430
Query	2763	CGAGTGGTTTTCGG*****ag*****G	2795
Sbjct	12455431	CGAGTGGTTTTCGGAAAAAAAAAAGAAAAAAG	12455463

Features in this part of subject sequence:

butyrophilin, subfamily 2, member A1 isoform 1 precursor  
butyrophilin, subfamily 2, member A1 isoform 2 precursorScore = 41.0 bits (44), Expect = 7.5  
Identities = 30/35 (85%), Gaps = 0/35 (0%)  
Strand=Plus/Plus

Query 2048 ACCTGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082

7/16/08


Query	725	CTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	784
Sbjct	17883984	CTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	17884043
Query	785	CGCCGCCTCCTCCAAGCCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGCGGGGGCGG	844
Sbjct	17884044	CGCCGCCTCCTCCAAGCCGGGGGAGAAGGGAGACAAGGTCGGTGGCAGTGGCGGGGGCGG	17884103
Query	845	CCATGGGGGCGGCGGCGGCGGGAGCAG	874
Sbjct	17884104	CCATGGGGGCGGCGGCGGCGGGAGCAG	17884133

Features in this part of subject sequence:

SRY (sex determining region Y)-box 4

Score = 1487 bits (1648), Expect = 0.0  
Identities = 829/831 (99%), Gaps = 1/831 (0%)  
Strand=Plus/Plus

Query	1966	TCCCATCCCCACCTTCCCGGGCCGGGGACCCACTCTGCCAGCCGGAGGGACGCGGAGG	2025
Sbjct	17884827	TCCCATCCCCACCTTCCCGGGCCGGGGACCCACTCTGCCAGCCGGAGGGACGCGGAGG	17884886
Query	2026	AGGAAGAGGGTAGACAGGGGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA	2085
Sbjct	17884887	AGGAAGAGGGTAGACAGGGGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA	17884946
Query	2086	-----GCGACTTCGAGTTTGCTCCCCCTTTGCTTGAAGAGACCCCTCCCCCTTC	2144
Sbjct	17884947	AAAAAAAAAAGCGACTTCGAGTTTGCTCCCCCTTTGCTTGAAGAGACCCCTCCCCCTTC	17885006
Query	2145	CAACGAGCTTCCGGACTTGCTGACACCCCGAGCAAGAAGGCGAGTTAGTTTTCTAGAGAC	2204
Sbjct	17885007	CAACGAGCTTCCGGACTTGCTGACACCCCGAGCAAGAAGGCGAGTTAGTTTTCTAGAGAC	17885066
Query	2205	TTGAAGGAGTCTCCCCCTTCTGTCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGG	2264
Sbjct	17885067	TTGAAGGAGTCTCCCCCTTCTGTCATCACCACCTTGGTTTTGTTTTATTTTGCTTCTTGG	17885126
Query	2265	TCAAGAAAGGAGGGGAGAACCCAGCGCACCCCTCCCCCCTTTTTTAAACGCGTGATGA	2324
Sbjct	17885127	TCAAGAAAGGAGGGGAGAACCCAGCGCACCCCTCCCCCCTTTTTTAAACGCGTGATGA	17885186
Query	2325	AGACAGAAGGCTCCGGGGTGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGG	2384
Sbjct	17885187	AGACAGAAGGCTCCGGGGTGACGAATTTGGCCGATGGCAGATGTTTTGGGGGAACGCCGG	17885246
Query	2385	GACTGAGAGACTCCACGCAGGCGAATTTCCCGTTTGGGGCCTCCCCCTCCTTTTTC	2444
Sbjct	17885247	GACTGAGAGACTCCACGCAGGCGAATTTCCCGTTTGGGGCCTCCCCCTCCTTTTTC	17885306
Query	2445	CCCTTGCCCCCTCTGCAGCCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGA	2504
Sbjct	17885307	CCCTTGCCCCCTCTGCAGCCGGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGA	17885366
Query	2505	CCGGCGCTAGGAAATGACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCG	2564
Sbjct	17885367	CCGGCGCTAGGAAATGACCCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCG	17885426
Query	2565	GGGGCGGAGGAGGACACGAACCTGGAAGGGGGTTACGGTCAAACCTGAAATGGATTTCAC	2624
Sbjct	17885427	GGGGCGGAGGAGGACACGAACCTGGAAGGGGGTTACGGTCAAACCTGAAATGGATTTCAC	17885486
Query	2625	GTTGGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGT	2684
Sbjct	17885487	GTTGGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGT	17885546
Query	2685	GAGGTGAGACTTCCCAGACCCCGGAGGCGTGGAGGAGAGGAGACTGTTTGATGTGGTACA	2744
Sbjct	17885547	GAGGTGAGACTTCCCAGACCCCGGAGGCGTGGAGGAGAGGAGACTGTTTGATGTGGTACA	17885606
Query	2745	GGGGCAGTCAGTGGAGGGCGAGTGGTTTCGGAAAAAGGAAAAAG	2795
Sbjct	17885607	GGGGCAGTCAGTGGAGGGCGAGTGGTTTCGGAAAAAGGAAAAAG	17885657

>ref|NW\_001838765.1|Hs2\_WGA158\_36  Homo sapiens chromosome 2 genomic contig, alternate asse  
(based on HuRef SCAF\_1103279188139)  
Length=2797789

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY-box 11

Score = 309 bits (342), Expect = 1e-80  
Identities = 224/259 (86%), Gaps = 0/259 (0%)  
Strand=Plus/Plus


Query	491	CGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCAT	550
Sbjct	719581	CGACCCAGACTGGTGCAAGACGGCGTCGGGCCACATCAAGCGGCCGATGAACGCGTTCAT	719640
Query	551	GGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCACATGCACAACGC	610
Sbjct	719641	GGTATGGTCCAAGATCGAACGCAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC	719700
Query	611	CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC	670
Sbjct	719701	CGAGATCTCCAAGAGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGAGAAGATCCC	719760
Query	671	TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAA	730
Sbjct	719761	GTTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCCGACTACCCCGACTACAA	719820
Query	731	GTACCGGCCCAGGAAGAAG	749
Sbjct	719821	GTACCGGCCCCGAAAAAG	719839

Features in this part of subject sequence:

SRY-box 11

Score = 131 bits (144), Expect = 5e-27  
Identities = 96/112 (85%), Gaps = 0/112 (0%)  
Strand=Plus/Plus

Query	1671	GGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGA	1730
Sbjct	720692	GGCTCCCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCGCGGGG	720751
Query	1731	GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTACCTACTGAAGGGCGC	1782
Sbjct	720752	GACTGGCTGGAGGCGAATTCTCCGACCTGGTGTTCACATATTGAAAGGCGC	720803

>ref|NT\_005334.15|Hs2\_5491  Homo sapiens chromosome 2 genomic contig, reference assembly  
Length=11088087

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY-box 11

Score = 309 bits (342), Expect = 1e-80  
Identities = 224/259 (86%), Gaps = 0/259 (0%)  
Strand=Plus/Plus

Query	491	CGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCAT	550
Sbjct	667099	CGACCCAGACTGGTGCAAGACGGCGTCGGGCCACATCAAGCGGCCGATGAACGCGTTCAT	667158
Query	551	GGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCACATGCACAACGC	610
Sbjct	667159	GGTATGGTCCAAGATCGAACGCAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC	667218
Query	611	CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC	670
Sbjct	667219	CGAGATCTCCAAGAGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGAGAAGATCCC	667278
Query	671	TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAA	730
Sbjct	667279	GTTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCCGACTACCCCGACTACAA	667338
Query	731	GTACCGGCCCAGGAAGAAG	749




Sbjct 667339 GTACCGGCCCGGAAAAAG 667357

Features in this part of subject sequence:  
SRY-box 11

Score = 131 bits (144), Expect = 5e-27  
Identities = 96/112 (85%), Gaps = 0/112 (0%)  
Strand=Plus/Plus

Query 1671 GGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGA 1730  
|||||  
Sbjct 668210 GGCTCCCACCTTCGAGTTCCCGGACTACTGCACGCGGAGCTGAGCGAGATGATCGCGGGG 668269  
Query 1731 GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTCACCTACTGAAGGGCGC 1782  
|||||  
Sbjct 668270 GACTGGCTGGAGGCGAAGTTCTCCGACCTGGTGTTCACATATTGAAAGGCGC 668321

>ref|NW\_001838652.1|Hs20\_WGA1211\_36  Homo sapiens chromosome 20 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188366)  
Length=22415471

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 12

Score = 291 bits (322), Expect = 3e-75  
Identities = 213/246 (86%), Gaps = 1/246 (0%)  
Strand=Plus/Plus

Query 494 CCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT 553  
|||||  
Sbjct 258081 CCCG-GCTGGTGCAAGACCCCGAGCGGCCACATCAAGAGGCCGATGAACGCATTTCATGGT 258139  
Query 554 GTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACATGCACAACGCCGA 613  
|||||  
Sbjct 258140 GTGGTCGCAGCACGAACGGCGGAAGATCATGGACCAGTGGCCCCGACATGCACAACGCCGA 258199  
Query 614 GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT 673  
|||||  
Sbjct 258200 GATCTCCAAGCGCCTGGGCCGCCGCTGGCAGCTGCTGCAGGACTCGGAGAAGATCCCGTT 258259  
Query 674 CATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA 733  
|||  
Sbjct 258260 CGTGGGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA 258319  
Query 734 CCGGCC 739  
|||||  
Sbjct 258320 CCGGCC 258325

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 12

Score = 131 bits (144), Expect = 5e-27  
Identities = 90/102 (88%), Gaps = 0/102 (0%)  
Strand=Plus/Plus

Query 1674 TCGCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733  
|||||  
Sbjct 258840 TCGCACTTCGAGTTCCCGGACTACTGCACCCCCGAGGTTACCGAGATGATCGCGGGGGAC 258899  
Query 1734 TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTCACCTACTGA 1775  
|||||  
Sbjct 258900 TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTTCACCTACTGA 258941

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 9967415   CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9967377
```

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 9967421   CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9967383
```

Features in this part of subject sequence:  
similar to hCG2045825


Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 9967427   CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9967389
```

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 9967433   CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9967395
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>ref|NT\_011387.8|Hs20\_11544  Homo sapiens chromosome 20 genomic contig, reference assembly  
Length=26259569

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 12

Score = 291 bits (322), Expect = 3e-75  
Identities = 213/246 (86%), Gaps = 1/246 (0%)  
Strand=Plus/Plus

```
Query 494      CCCGAGCTGGTGCAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT 553
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 246656   CCCG-GCTGGTGCAGACCCCGAGCGGCCACATCAAGAGGCCGATGAACGCATTTCATGGT 246714

Query 554      GTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCACATGCACAACGCCGA 613
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 246715   GTGGTCGCAGCACGAACGGCGGAAGATCATGGACCAGTGGCCCACATGCACAACGCCGA 246774

Query 614      GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT 673
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 246775   GATCTCCAAGCGCCTGGGCCGCCGCTGGCAGCTGCTGCAGGACTCGGAGAAGATCCCGTT 246834

Query 674      CATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA 733
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 246835   CGTGCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA 246894

Query 734      CCGGCC 739
                |||||
Sbjct 246895   CCGGCC 246900
```

Features in this part of subject sequence:

SRY (sex determining region Y)-box 12

Score = 131 bits (144), Expect = 5e-27  
Identities = 90/102 (88%), Gaps = 0/102 (0%)  
Strand=Plus/Plus

```
Query 1674      TCGCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733
                ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Sbjct 247415     TCGCACTTCGAGTTCCCGGACTACTGCACCCCCGAGGTTACCGAGATGATCGCGGGGAC 247474

Query 1734      TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTTCACCTACTGA 1775
                ||||| | ||| ||||||| ||| ||||||| ||||||| |||
Sbjct 247475     TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTTCACCTACTGA 247516
```

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||||| ||||||| ||||||| ||| ||||||| ||||||| |||
Sbjct 9955587    CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955549
```

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||||| ||||||| ||||||| ||| ||||||| ||||||| |||
Sbjct 9955593    CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955555
```

Features in this part of subject sequence:  
similar to hCG2045825


Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||||| ||||||| ||||||| ||| ||||||| ||||||| |||
Sbjct 9955599    CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955561
```

Features in this part of subject sequence:  
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Minus

```
Query 1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                ||||||| ||||||| ||||||| ||| ||||||| ||||||| |||
Sbjct 9955605    CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955567
```

>ref|NW\_001838084.2|Hs13\_WGA793\_36  Homo sapiens chromosome 13 genomic contig, alternate as  
(based on HuRef SCAF\_1103279188152)  
Length=25468656

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY-box 21

Score = 140 bits (154), Expect = 1e-29  
Identities = 164/219 (74%), Gaps = 2/219 (0%)

Strand=Plus/Plus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC 581
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 16996200 CACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGTCGCGGGCTCAGCGGCGCAAGATG 16996259

Query 582 ATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGG 641
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct 16996260 GCCCAGGAGAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCTTGGGCGCCGAGTGG 16996319


Query 642 AAGCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCT 700
      || ||||| ||||| || || || || || || || || || || || || || || || ||
Sbjct 16996320 AAAGTGTCTACAGAGTCGGAGAAGCGGCCGTTCA-TCGACGAGGCCAAGCGTCTACGCGC 16996378

Query 701 CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
      || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 16996379 CATGCACATGAAGGAGCACCCCGACTACAAGTACCGGCC 16996417
```

Features in this part of subject sequence:  
hypothetical protein

Score = 42.8 bits (46), Expect = 2.2  
Identities = 28/31 (90%), Gaps = 0/31 (0%)  
Strand=Plus/Minus

```
Query 2050 CTGTGATTGTTGTTATTGATGTTGTTGTTGA 2080
      ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1920740 CTGTGGTTGTTGTTGTTGTTGTTGTTGTTGA 1920710
```

>ref|NT\_009952.14|Hs13\_10109  Homo sapiens chromosome 13 genomic contig, reference assembly  
Length=25443670

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY-box 21

Score = 140 bits (154), Expect = 1e-29  
Identities = 164/219 (74%), Gaps = 2/219 (0%)  
Strand=Plus/Minus

```
Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC 581
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 8453961 CACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGTCGCGGGCTCAGCGGCGCAAGATG 8453902

Query 582 ATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGG 641
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct 8453901 GCCCAGGAGAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCTTGGGCGCCGAGTGG 8453842


Query 642 AAGCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCT 700
      || ||||| ||||| || || || || || || || || || || || || || || || ||
Sbjct 8453841 AAAGTGTCTACAGAGTCGGAGAAGCGGCCGTTCA-CGACGAGGCCAAGCGTCTACGCGC 8453783

Query 701 CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
      || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 8453782 CATGCACATGAAGGAGCACCCCGACTACAAGTACCGGCC 8453744
```

Features in this part of subject sequence:  
insulin receptor substrate 2  
hypothetical protein

Score = 42.8 bits (46), Expect = 2.2  
Identities = 28/31 (90%), Gaps = 0/31 (0%)  
Strand=Plus/Plus

```
Query 2050 CTGTGATTGTTGTTATTGATGTTGTTGTTGA 2080
      ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 23527988 CTGTGGTTGTTGTTGTTGTTGTTGTTGTTGA 23528018
```

>ref|NW\_001838403.1|Hs17\_WGA1112\_36  Homo sapiens chromosome 17 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188371)  
Length=15048748

Features in this part of subject sequence:  
SRY-box 15


Score = 129 bits (142), Expect = 2e-26  
Identities = 158/213 (74%), Gaps = 2/213 (0%)  
Strand=Plus/Minus

```
Query  528      AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA  586
          ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7078179  AAGCGGCCGATGAACGCGTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA  7078121

Query  587      GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT  646
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7078120  GCAGAACCCCAAGATGCACAACCTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGGAAGCT  7078061

Query  647      GCTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA  706
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7078060  GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA  7078001

Query  707      CATGGCTGACTACCCCGACTACAAGTACCGGCC  739
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7078000  CCTGCGCGACTACCCCGACTACAAGTACCGGCC  7077968
```

>ref|NT\_010718.15|Hs17\_10875  Homo sapiens chromosome 17 genomic contig, reference assembly  
Length=21163833

Features in this part of subject sequence:  
SRY-box 15


Score = 129 bits (142), Expect = 2e-26  
Identities = 158/213 (74%), Gaps = 2/213 (0%)  
Strand=Plus/Minus

```
Query  528      AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA  586
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7090195  AAGCGGCCGATGAACGCGTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA  7090137

Query  587      GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT  646
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7090136  GCAGAACCCCAAGATGCACAACCTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGGAAGCT  7090077

Query  647      GCTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA  706
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7090076  GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA  7090017

Query  707      CATGGCTGACTACCCCGACTACAAGTACCGGCC  739
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  7090016  CCTGCGCGACTACCCCGACTACAAGTACCGGCC  7089984
```

>ref|NW\_001838454.2|Hs17\_WGA1163\_36  Homo sapiens chromosome 17 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188168)  
Length=12595466

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
transcription factor SOX9

Score = 104 bits (114), Expect = 8e-19  
Identities = 96/122 (78%), Gaps = 0/122 (0%)  
Strand=Plus/Minus

```
Query  521      GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT  580
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  5396434  GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCGCAGGCGGCGCGCAGGAAGCT  5396375

Query  581      CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG  640
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  5396374  CGCGGACCAGTACCCGCACTTGACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTCTG  5396315

Query  641      GA  642
          ||
Sbjct  5396314  GA  5396313
```



Score = 91.5 bits (100), Expect = 5e-15  
Identities = 153/219 (69%), Gaps = 2/219 (0%)  
Strand=Plus/Minus

```
Query  526      TCAAGCGACCCATGAACGCCTTCATGGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGG  585
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  12593937  TCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCC  12593878

Query  586      AGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGC  645
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Sbjct  12593877  AGGAGAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAC  12593818

Query  646      TGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCTCAAG  704
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Sbjct  12593817  TTTTGTCTGGAGACGGAGAAGCGGCCGTTCA-TCGACGAGGCTAAGCGGCTGCGAGCGCTG  12593759

Query  705      CACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG  743
          |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Sbjct  12593758  CACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGG  12593720
```

Features flanking this part of subject sequence:

368249 bp at 5' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isoform...  
1716439 bp at 3' side: hypothetical protein LOC205428

Score = 46.4 bits (50), Expect = 0.18  
Identities = 31/35 (88%), Gaps = 0/35 (0%)  
Strand=Plus/Plus

```
Query  2228      CATCACACCTTGGTTTTGTTTTATTTTGCTTCTT  2262
          |||||  ||  |||||  |||||  |||||  |||||  |||||
Sbjct  48631837  CATCATCACTTTGGTTATGTTTTATTTTGCTTCTT  48631871
```

Features flanking this part of subject sequence:

555396 bp at 5' side: similar to peptidylprolyl isomerase A-like  
680809 bp at 3' side: butyrylcholinesterase precursor

Score = 42.8 bits (46), Expect = 2.2  
Identities = 26/28 (92%), Gaps = 0/28 (0%)  
Strand=Plus/Plus

```
Query  2055      ATTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||  |||||  ||  |||||  |||||  |||||
Sbjct  27830621  ATTGTTGTTGTTGTTGTTGTTGTTGATG  27830648
```

Features flanking this part of subject sequence:

8911 bp at 5' side: sterile alpha motif domain containing 7  
40774 bp at 3' side: leucine rich repeat containing 31

Score = 41.0 bits (44), Expect = 7.5  
Identities = 31/37 (83%), Gaps = 0/37 (0%)  
Strand=Plus/Plus


```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAA  2092
          |||||  |||||  |||||  |||||  ||  |||||  ||
Sbjct  24430482  TTGTTGTTATTGTTGTTGTTGTTGTTCTGAAAAATAA  24430518
```

Features flanking this part of subject sequence:

360070 bp at 5' side: similar to hCG2021878  
1305561 bp at 3' side: hypothetical protein LOC131149

Score = 41.0 bits (44), Expect = 7.5  
Identities = 33/40 (82%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

```
Query  180      TTCTCTCTTTACCCACCTCCGCCCTGCGAGGAGTTGAGG  219
          |||||  |||||  ||  ||  |||||  ||  |||||
Sbjct  31502884  TTCTCTCTTTACACCACTCAGCCGCTGCCAGGGGTTGAGG  31502845
```

>ref|NT\_010641.15|Hs17\_10798  Homo sapiens chromosome 17 genomic contig, reference assembly  
Length=11472733

Sort alignments for this subject seq  
E value Score Percent identity







40760 bp at 5' side: leucine rich repeat containing 31  
8896 bp at 3' side: sterile alpha motif domain containing 7

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAAAA	2092
Sbjct	76123541	TTGTTGTTATTGTTGTTGTTGTTGTTCTGAAAAATAA	76123505

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Query	528	AAGCGACCCATGAACGCCCTTCATGGTGTGGTCTGCAGATCGAGCGGCGCAAGAT---CATG	584
Sbjct	3649310	AAACGGCCCATGAACGCCCTTCATGGTATGGTCCC GCGGGCAGCGGCGCAAAATGGCCCTG	3649251
Query	585	GAGCAGTCGCCCCACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAG	644
Sbjct	3649250	GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA	3649194
Query	645	CTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCTCAA	703
Sbjct	3649193	CTGCTGACC GACGCCGAGAAGCGACCATT CAT-CGACGAGGCCAAGCGACTTCGCGCCGT	3649135
Query	704	GCACATGGCTGACTACCCCGACTACAAGTACCGGCC	739
Sbjct	3649134	GCACATGAAGGAGTATCCGGACTACAAGTACCGACC	3649099

166860 bp at 5' side: zinc finger protein of the cerebellum 3  
893562 bp at 3' side: fibroblast growth factor 13 isoform 1A

Query	2048	ACCTGTGATTGTTGTTATTGATGTTGTTGTTG	2079
Sbjct	882950	ACCTGTGATAGTTTTTGTGTTGTTGTTGTTG	882981

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGAT---CATG	584
Sbjct	23798156	AAACGGCCCATGAACGCCTTCATGGTATGGTCCCGCGGGCAGCGGCGCAAATGGCCCTG	23798097
Query	585	GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAG	644

```
Sbjct  23798096  GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA 23798040
Query   645      CTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAA 703
Sbjct  23798039  CTGCTGACCGACGCCGAGAAGCGACCATTTCAT-CGACGAGGCCAAGCGACTTCGCGCCGT 23797981
Query   704      GCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
Sbjct  23797980  GCACATGAAGGAGTATCCGGACTACAAGTACCGACC 23797945
```

Features in this part of subject sequence:  
dedicator of cytokinesis 11

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query   1149      GCCTCGGCCTCCGCCTCCTCGGCAGCC 1175
Sbjct  1898025  GCCTCCGCCTCCGCCTCCTCCGCAGCC 1897999
```

Features flanking this part of subject sequence:  
1062887 bp at 5' side: glutamate dehydrogenase 2  
1072247 bp at 3' side: glutamate receptor 3 isoform flop precursor


Score = 41.0 bits (44), Expect = 7.5  
Identities = 33/40 (82%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaaaaaaaaa 2095
Sbjct  5457504  TTGTTGTTGTTGTTGTTGTTGTTGTTTTCAGAAAAACAAA 5457465
```

Features flanking this part of subject sequence:  
168026 bp at 5' side: zinc finger protein of the cerebellum 3  
894725 bp at 3' side: fibroblast growth factor 13 isoform 1B

Score = 41.0 bits (44), Expect = 7.5  
Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

```
Query   2048      ACCTGTGATTGTTGTTATTGATGTTGTTGTTG 2079
Sbjct  21031603  ACCTGTGATAGTTTTTGTGTTGTTGTTGTTGTTG 21031634
```

>ref|NT\_027140.6|Hs13\_27300  Homo sapiens chromosome 13 genomic contig, reference assembly  
Length=1821999

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 1

Score = 96.9 bits (106), Expect = 1e-16  
Identities = 152/215 (70%), Gaps = 2/215 (0%)  
Strand=Plus/Plus

```
Query   526      TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG 585
Sbjct  218130  TCAAACGGCCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCC 218189
Query   586      AGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGC 645
Sbjct  218190  AGGAGAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCCTGGGGGCCGAGTGGAAGG 218249
Query   646      TGCTCAAAGACAGCGACAAGATCCCTTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG 704
Sbjct  218250  TCATGTCCGAGGCCGAGAAGCGGCCGTTCA-TCGACGAGGCCAAGCGGCTGCGCGCGCTG 218308
Query   705      CACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
```


Sbjct 218309 CACATGAAGGAGCACCCGGATTACAAGTACCGGCC 218343

Features flanking this part of subject sequence:

269051 bp at 5' side: SRY (sex determining region Y)-box 1  
38475 bp at 3' side: hypothetical protein LOC122258

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	488205	TTGTTGTTGTTGATGTTGTTGTTGTTG	488231

>ref|NW\_001838745.1|Hs22\_WGA1304\_36  Homo sapiens chromosome 22 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188372)  
Length=21026802

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 10

Score = 95.1 bits (104), Expect = 4e-16  
Identities = 94/122 (77%), Gaps = 0/122 (0%)  
Strand=Plus/Minus

Query	521	GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT	580
Sbjct	16472614	GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT	16472555
Query	581	CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG	640
Sbjct	16472554	CGCGGACCAGTACCCGCACCTGCACAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG	16472495
Query	641	GA	642
Sbjct	16472494	GA	16472493

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 10

Score = 77.0 bits (84), Expect = 1e-10  
Identities = 79/101 (78%), Gaps = 2/101 (1%)  
Strand=Plus/Minus

Query	644	GCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCGAG-AGGCGGAGCGGCTGCGCCTCA	702
Sbjct	16467270	GCTGCTGAACGAAAGTGACAAGCGCCCCTTCAT-CGAGGAGGCTGAGCGGCTCCGTATGC	16467212
Query	703	AGCACATGGCTGACTACCCCGACTACAAGTACCGGCCAGG	743
Sbjct	16467211	AGCACAAGAAAGACCACCCGGACTACAAGTACCAGCCCAGG	16467171

Features flanking this part of subject sequence:  
22174 bp at 5' side: like-glycosyltransferase  
1289151 bp at 3' side: intestine-specific homeobox

Score = 42.8 bits (46), Expect = 2.2  
Identities = 25/26 (96%), Gaps = 0/26 (0%)  
Strand=Plus/Plus


Query	2056	TTGTTGTTATTGATGTTGTTGTTGAT	2081
Sbjct	12263566	TTGTTGTTATTGTTGTTGTTGTTGAT	12263591

Features in this part of subject sequence:  
calcineurin binding protein 1

Score = 41.0 bits (44), Expect = 7.5

Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGGCAAA  2087
          |||||
Sbjct  2585440    TTGTTGTTGTTGTTGTTGTTGTTGTTGGTAAA  2585471
```

>ref|NT\_011520.11|Hs22\_11677  Homo sapiens chromosome 22 genomic contig, reference assembly  
Length=23276302

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 10

Score = 95.1 bits (104), Expect = 4e-16  
Identities = 94/122 (77%), Gaps = 0/122 (0%)  
Strand=Plus/Minus

```
Query  521      GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT  580
          |||||
Sbjct  17770001   GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT  17769942

Query  581      CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG  640
          |||||
Sbjct  17769941   CGCGGACCAGTACCCGCACCTGCACAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG  17769882

Query  641      GA      642
          ||
Sbjct  17769881   GA      17769880
```

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 10

Score = 77.0 bits (84), Expect = 1e-10  
Identities = 79/101 (78%), Gaps = 2/101 (1%)  
Strand=Plus/Minus

```
Query  644      GCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCGAG-AGGCGGAGCGGCTGCGCCTCA  702
          |||||
Sbjct  17764657   GCTGCTGAACGAAAGTGACAAGCGCCCCTTCAT-CGAGGAGGCTGAGCGGCTCCGTATGC  17764599

Query  703      AGCACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG  743
          |||||
Sbjct  17764598   AGCACAAGAAAGACCACCCGGACTACAAGTACCAGCCCAGG  17764558
```

Features flanking this part of subject sequence:  
22175 bp at 5' side: like-glycosyltransferase  
1283418 bp at 3' side: intestine-specific homeobox


Score = 42.8 bits (46), Expect = 2.2  
Identities = 25/26 (96%), Gaps = 0/26 (0%)  
Strand=Plus/Plus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGAT  2081
          |||||
Sbjct  13570207   TTGTTGTTATTGTTGTTGTTGTTGAT  13570232
```

Features in this part of subject sequence:  
calcineurin binding protein 1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGGCAAA  2087
          |||||
Sbjct  3900601    TTGTTGTTGTTGTTGTTGTTGTTGTTGGTAAA  3900632
```

>ref|NW\_001839122.2|Hs8\_WGA515\_36  Homo sapiens chromosome 8 genomic contig, alternate asse  
(based on HuRef SCAF 1103279188150)

Length=4000776

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY-box 7

Score = 87.8 bits (96), Expect = 6e-14  
Identities = 63/72 (87%), Gaps = 3/72 (4%)  
Strand=Plus/Plus


```
Query 681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC- 739
                |||
Sbjct 1473842  GAGGCGGAGCGGCTGCGCCTGCAGCACATGCAGGACTACCCCAACTACAAGTACCGGCCG 1473901
                |||
Query 740      --CAGGAAGAAG 749
                |||
Sbjct 1473902  CGCAGGAAGAAG 1473913
```

Features in this part of subject sequence:

SRY-box 7

Score = 53.6 bits (58), Expect = 0.001  
Identities = 73/102 (71%), Gaps = 0/102 (0%)  
Strand=Plus/Plus

```
Query 530      GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCA 589
                |||
Sbjct 1470162  GCGGCCCATGAACGCCTTCATGGTTTGGGCCAAGGACGAGAGGAAACGGCTGGCAGTGCA 1470221
                |||
Query 590      GTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG 631
                |||
Sbjct 1470222  GAACCCGGACCTGCACAACGCCGAGCTCAGCAAGATGCTGGG 1470263
```

>ref|NT\_077531.3|Hs8\_77580  Homo sapiens chromosome 8 genomic contig, reference assembly  
Length=4537293

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY-box 7

Score = 87.8 bits (96), Expect = 6e-14  
Identities = 63/72 (87%), Gaps = 3/72 (4%)  
Strand=Plus/Minus


```
Query 681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC- 739
                |||
Sbjct 3059477  GAGGCGGAGCGGCTGCGCCTGCAGCACATGCAGGACTACCCCAACTACAAGTACCGGCCG 3059418
                |||
Query 740      --CAGGAAGAAG 749
                |||
Sbjct 3059417  CGCAGGAAGAAG 3059406
```

Features in this part of subject sequence:

SRY-box 7

Score = 53.6 bits (58), Expect = 0.001  
Identities = 73/102 (71%), Gaps = 0/102 (0%)  
Strand=Plus/Minus

```
Query 530      GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCA 589
                |||
Sbjct 3063157  GCGGCCCATGAACGCCTTCATGGTTTGGGCCAAGGACGAGAGGAAACGGCTGGCAGTGCA 3063098
                |||
Query 590      GTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG 631
                |||
Sbjct 3063097  GAACCCGGACCTGCACAACGCCGAGCTCAGCAAGATGCTGGG 3063056
```

>ref|NW\_001838339.2|Hs16\_WGA937\_36  Homo sapiens chromosome 16 genomic contig, alternate as

(based on HuRef SCAF\_1103279188181)  
Length=2624016

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 8


Score = 86.0 bits (94), Expect = 2e-13  
Identities = 83/107 (77%), Gaps = 0/107 (0%)  
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG	587
Sbjct	1665887	AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGGCGCGCCGCAAGCTGGCCGAC	1665828
Query	588	CAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA	634
Sbjct	1665827	CAGTACCCGCACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAA	1665781

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 8

Score = 53.6 bits (58), Expect = 0.001  
Identities = 71/99 (71%), Gaps = 6/99 (6%)  
Strand=Plus/Minus

Query	681	GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC-----	734
Sbjct	1664351	GAGGCAGAGCGCCTTCGCGTGCAGCACAAGAAGGACCACCCCGACTACAAGTACCAGCCA	1664292
Query	735	CGGCCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCC	773
Sbjct	1664291	CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC	1664253

>ref|NT\_037887.4|Hs16\_37891  Homo sapiens chromosome 16 genomic contig, reference assembly  
Length=8576922

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 8


Score = 86.0 bits (94), Expect = 2e-13  
Identities = 83/107 (77%), Gaps = 0/107 (0%)  
Strand=Plus/Plus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG	587
Sbjct	972230	AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGGCGCGCCGCAAGCTGGCCGAC	972289
Query	588	CAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA	634
Sbjct	972290	CAGTACCCGCACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAA	972336

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 8

Score = 53.6 bits (58), Expect = 0.001  
Identities = 71/99 (71%), Gaps = 6/99 (6%)  
Strand=Plus/Plus

Query	681	GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC-----	734
Sbjct	973766	GAGGCAGAGCGCCTTCGCGTGCAGCACAAGAAGGACCACCCCGACTACAAGTACCAGCCA	973825
Query	735	CGGCCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCC	773
Sbjct	973826	CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC	973864

>ref|NW\_001838533.2|Hs1\_WGA129\_36  Homo sapiens chromosome 1 genomic contig, alternate asse  
(based on HuRef SCAF\_1103279188157)  
Length=37103761

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY-box 13

Score = 77.0 bits (84), Expect = 1e-10  
Identities = 73/91 (80%), Gaps = 2/91 (2%)  
Strand=Plus/Minus

Query	522	CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC	581
Sbjct	1847108	CACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATC	1847049
Query	582	ATGGA-GCAGTCGCCCCGACATGCACAACGCC	611
Sbjct	1847048	CTGCAAGCCTTC-CCAGACATGCACAACCTCC	1847019

Features in this part of subject sequence:  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18  
Identities = 34/40 (85%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaaaaaaaaa	2095
Sbjct	3618816	TTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAAAAAA	3618777

Features in this part of subject sequence:  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18  
Identities = 34/40 (85%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaaaaaaaaa	2095
Sbjct	3618819	TTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAAAAAA	3618780

Features flanking this part of subject sequence:  
76699 bp at 5' side: chromosome 1 open reading frame 21  
327829 bp at 3' side: hypothetical protein LOC116461

Score = 42.8 bits (46), Expect = 2.2  
Identities = 26/28 (92%), Gaps = 0/28 (0%)  
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGG	2083
Sbjct	21499677	TTGTTGTTGTTGTTGTTGTTGTTGTTGATGG	21499650

Features flanking this part of subject sequence:  
1296333 bp at 5' side: regulator of G-protein signalling 18  
409014 bp at 3' side: family with sequence similarity 5, member C

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	15037624	TTGTTGTTATTGTTGTTGTTGTTGTTGTTG	15037598

Features in this part of subject sequence:





```
Query 582 ATG-GAGCAGTCGCCCCGACATGCACAACGCC 611
      || ||| || || ||||| ||||| ||
Sbjct 54583238 CTGCAAGCCTTC-CCAGACATGCACAACCTCC 54583267
```

Features in this part of subject sequence:

protein phosphatase 1, regulatory (inhibitor) subunit 12B...  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18  
Identities = 34/40 (85%), Gaps = 0/40 (0%)  
Strand=Plus/Plus

```
Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaaaaaa 2095
      ||||| ||| ||||| ||||| || ||||| ||
Sbjct 52810695 TTGTTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAA 52810734
```

Features in this part of subject sequence:

protein phosphatase 1, regulatory (inhibitor) subunit 12B...  
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18  
Identities = 34/40 (85%), Gaps = 0/40 (0%)  
Strand=Plus/Plus

```
Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaaaaaa 2095
      ||||| ||| ||||| ||||| || ||||| ||
Sbjct 52810698 TTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAA 52810737
```

Features flanking this part of subject sequence:

327837 bp at 5' side: hypothetical protein LOC116461  
76799 bp at 3' side: chromosome 1 open reading frame 21

Score = 42.8 bits (46), Expect = 2.2  
Identities = 26/28 (92%), Gaps = 0/28 (0%)  
Strand=Plus/Plus

```
Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGG 2083
      ||||| ||| ||||| ||||| ||
Sbjct 34860172 TTGTTGTTGTTGTTGTTGTTGTTGATGG 34860199
```

Features in this part of subject sequence:

astrotactin isoform 1  
astrotactin isoform 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 22/22 (100%), Gaps = 0/22 (0%)  
Strand=Plus/Minus

```
Query 2290 GCACCCCTccccccobtttttt 2311
      ||||| ||||| ||||| ||||| ||
Sbjct 27602408 GCACCCCTCCCCCCTTTTTTT 27602387
```

Features in this part of subject sequence:

hypothetical protein

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query 2423 CCTttttttCCTCCCTCTTTTCCCCTT 2449
      || ||||| ||| ||||| ||||| ||
Sbjct 28014783 CCATTTTTTCTGCCTCTTTTCCCCTT 28014757
```

Features flanking this part of subject sequence:

409150 bp at 5' side: family with sequence similarity 5, member C  
1294572 bp at 3' side: regulator of G-protein signalling 18

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus


```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 41323524  TTGTTGTTATTGTTGTTGTTGTTGTTG 41323550
```

Features flanking this part of subject sequence:

409171 bp at 5' side: family with sequence similarity 5, member C  
1294551 bp at 3' side: regulator of G-protein signalling 18

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 41323545  TTGTTGTTATTGTTGTTGTTGTTGTTG 41323571
```

>ref|NW\_001839132.1|Hs8\_WGA525\_36  Homo sapiens chromosome 8 genomic contig, alternate asse  
(based on HuRef SCAF\_1103279188282)  
Length=30141836

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY-box 17

Score = 66.2 bits (72), Expect = 2e-07  
Identities = 50/59 (84%), Gaps = 0/59 (0%)  
Strand=Plus/Plus

```
Query 681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
                |||
Sbjct 7238558  GAGGCGGAGCGGCTGCGCGTGCAGCACATGCAGGACCACCCCAACTACAAGTACCGGCC 7238616
```

Features in this part of subject sequence:  
SRY-box 17

Score = 55.4 bits (60), Expect = 3e-04  
Identities = 76/105 (72%), Gaps = 6/105 (5%)  
Strand=Plus/Plus

```
Query 530      GCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATCATGG---A 586
                |||
Sbjct 7237795  GCGGCCGATGAACGCTTTCATGGTGTGGGCTAAGGACGA---GCGCAAGCGGCTGGCGCA 7237851

Query 587      GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG 631
                |||
Sbjct 7237852  GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGG 7237896
```

Features in this part of subject sequence:  
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 497262  TTGTTGTTATTGTTGTTGTTGTTGTTG 497288
```

Features in this part of subject sequence:  
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5  
Identities = 30/35 (85%), Gaps = 0/35 (0%)  
Strand=Plus/Plus

```
Query 2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA 2085
                |||
Sbjct 497266  TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTGACA 497300
```

Features flanking this part of subject sequence:

63747 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...  
181279 bp at 3' side: similar to hCG1799828

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus


```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||
Sbjct  27230124  TTGTTGTTATTGTTGTTGTTGTTGTTG  27230098
```

Features flanking this part of subject sequence:

473228 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1  
33133 bp at 3' side: hepatocyte nuclear factor 4, gamma

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||
Sbjct  28305493  TTGTTGTTGTTGTTGTTGTTGTTGATG  28305467
```

>ref|NT\_008183.18|Hs8\_8340  Homo sapiens chromosome 8 genomic contig, reference assembly  
Length=38454502

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY-box 17

Score = 66.2 bits (72), Expect = 2e-07  
Identities = 50/59 (84%), Gaps = 0/59 (0%)  
Strand=Plus/Plus

```
Query  681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC  739
          |||||
Sbjct  7225020  GAGGCAGAGCGGCTGCGCGTGCAGCACATGCAGGACCACCCCAACTACAAGTACCGGCC  7225078
```

Features in this part of subject sequence:  
SRY-box 17

Score = 55.4 bits (60), Expect = 3e-04  
Identities = 76/105 (72%), Gaps = 6/105 (5%)  
Strand=Plus/Plus

```
Query  530      GCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATCATGG---A  586
          |||
Sbjct  7224257  GCGGCCGATGAACGCCTTCATGGTGTGGGCTAAGGACGA---GCGCAAGCGGCTGGCGCA  7224313

Query  587      GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG  631
          |||||
Sbjct  7224314  GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGG  7224358
```

Features flanking this part of subject sequence:

63856 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...  
184610 bp at 3' side: similar to hCG1799828 isoform 1

Score = 42.8 bits (46), Expect = 2.2  
Identities = 31/36 (86%), Gaps = 0/36 (0%)  
Strand=Plus/Minus

```
Query  2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAA  2086
          |||
Sbjct  27193847  TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTAGCAA  27193812
```

Features in this part of subject sequence:  
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 488931    TTGTTGTTATTGTTGTTGTTGTTGTTG 488957
```

Features in this part of subject sequence:  
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5  
Identities = 30/35 (85%), Gaps = 0/35 (0%)  
Strand=Plus/Plus

```
Query 2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA 2085
                |||
Sbjct 488935    TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTGACA 488969
```

Features flanking this part of subject sequence:  
63869 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...  
184606 bp at 3' side: similar to hCG1799828 isoform 1


Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 27193851  TTGTTGTTATTGTTGTTGTTGTTGTTGTTG 27193825
```

Features flanking this part of subject sequence:  
474603 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1  
33122 bp at 3' side: hepatocyte nuclear factor 4, gamma

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct 28272460  TTGTTGTTGTTGTTGTTGTTGTTGTTGATG 28272434
```

>ref|NW\_001842422.1|HsY\_WGA1383\_36  Homo sapiens chromosome Y genomic contig, alternate ass  
(based on HuRef SCAF\_1103279188414)  
Length=3942718

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
sex determining region Y

Score = 64.4 bits (70), Expect = 7e-07  
Identities = 94/126 (74%), Gaps = 8/126 (6%)  
Strand=Plus/Minus


```
Query 528      AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT 583
                |||
Sbjct 8468      AAGCGACCCATGAACGCATTATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT 8410

Query 584      GGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA 643
                |||
Sbjct 8409      AGAG-AATC-CCAGA-ATGCGAACTCAGAGATCAGCAAGCAGCTGGGATACCACTGGAA 8353

Query 644      GCTGCT 649
                |||
Sbjct 8352      AATGCT 8347
```

Features flanking this part of subject sequence:



>ref|NT\_011333.5|Hs20\_11490  Homo sapiens chromosome 20 genomic contig, reference assembly  
Length=1702150

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
hypothetical protein  
SRY-box 18


Score = 62.6 bits (68), Expect = 2e-06  
Identities = 83/114 (72%), Gaps = 6/114 (5%)  
Strand=Plus/Minus

Query	521	GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT	580
Sbjct	1417251	GCGCATCCGGCGGCCCATGAACGCCTTCATGGTGTGGGCAAAGGACGA---GCGCAAGCG	1417195
Query	581	CATGG---AGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG	631
Sbjct	1417194	GCTGGCTCAGCAGAACCCGGACCTGCACAACGCGGTGCTCAGCAAGATGCTGGG	1417141

Features in this part of subject sequence:  
hypothetical protein  
SRY-box 18

Score = 53.6 bits (58), Expect = 0.001  
Identities = 47/59 (79%), Gaps = 0/59 (0%)  
Strand=Plus/Minus

Query	681	GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC	739
Sbjct	1416895	GAAGCCGAACGGCTGCGCGTGCAGCACTTGCGCGACCACCCCACTACAAGTACCGGCC	1416837

>ref|NW\_001838052.1|Hs12\_WGA761\_36  Homo sapiens chromosome 12 genomic contig, alternate as  
(based on HuRef SCAF\_1103279188408)  
Length=21675488

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 5 isoform c  
SRY (sex determining region Y)-box 5 isoform b

Score = 57.2 bits (62), Expect = 1e-04  
Identities = 76/103 (73%), Gaps = 2/103 (1%)  
Strand=Plus/Minus

Query	522	CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT	580
Sbjct	14103106	CACATAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT	14103048
Query	581	CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG	623
Sbjct	14103047	CCTTCAAGCCTTTCTGACATGCACAACCTCAACATCAGCAAG	14103005

Features flanking this part of subject sequence:  
15642 bp at 5' side: hypothetical protein LOC440087  
585 bp at 3' side: hypothetical protein LOC144608

Score = 42.8 bits (46), Expect = 2.2  
Identities = 29/33 (87%), Gaps = 0/33 (0%)  
Strand=Plus/Minus


Query	2050	CTGTGATTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	5384229	CTGTGTTTGTTGTTGTTGTTGTTGTTGTTGTTG	5384197

Features flanking this part of subject sequence:  
70138 bpat 5' side: pleckstrin homology domain containing, family A member 5

463 bp at 3' side: AE binding protein 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query 1144      CCAGCGCCTCGGCCTCCGCCTCCTC 1168
                ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 10001352  CCACCGCCTCGGCCTCCGCCTCCTC 10001328
```

>ref|NT\_009714.16|Hs12\_9871  Homo sapiens chromosome 12 genomic contig, reference assembly  
Length=27615668

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY (sex determining region Y)-box 5 isoform a  
SRY (sex determining region Y)-box 5 isoform b

Score = 57.2 bits (62), Expect = 1e-04  
Identities = 76/103 (73%), Gaps = 2/103 (1%)  
Strand=Plus/Minus

```
Query 522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT 580
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 16455227  CACATAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT 16455169

Query 581      CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG 623
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 16455168  CCTTCAAGCCTTTCCTGACATGCACAACTCCAACATCAGCAAG 16455126
```

Features flanking this part of subject sequence:

15639 bp at 5' side: hypothetical protein LOC440087  
585 bp at 3' side: hypothetical protein LOC144608

Score = 42.8 bits (46), Expect = 2.2  
Identities = 29/33 (87%), Gaps = 0/33 (0%)  
Strand=Plus/Minus

```
Query 2050      CTGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 7734259  CTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 7734227
```

Features in this part of subject sequence:  
pregnancy-zone protein

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus


```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
                ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 2067054  TTGTTGTTATTGTTGTTGTTGTTGTTGTTGTTG 2067080
```

Features flanking this part of subject sequence:

70051 bp at 5' side: pleckstrin homology domain containing, family A member 5  
462 bp at 3' side: AE binding protein 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query 1144      CCAGCGCCTCGGCCTCCGCCTCCTC 1168
                ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 12351770  CCACCGCCTCGGCCTCCGCCTCCTC 12351746
```

>ref|NW\_001838671.1|Hs20\_WGA1230\_36  Homo sapiens chromosome 20 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188118)  
Length=1477768





Features flanking this part of subject sequence:

1925 bp at 5' side: TRM1 tRNA methyltransferase 1  
16847 bp at 3' side: transcriptional repressor NAC1

Score = 51.8 bits (56), Expect = 0.004  
Identities = 34/38 (89%), Gaps = 0/38 (0%)  
Strand=Plus/Minus


```
Query 1149      GCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                |||||
Sbjct 4491977   GCCTCGGCCTCCGCCTCCGCAGCCTCCGCAGCCTCCGC 4491940
```

Features in this part of subject sequence:

calcium channel, alpha 1A subunit isoform 2  
calcium channel, alpha 1A subunit isoform 1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGA 2080
                |||||
Sbjct 4698340   TTGTTGTTGTTGATGTTGTTGTTGA 4698316
```

>ref|NT\_023133.12|Hs5\_23289  Homo sapiens chromosome 5 genomic contig, reference assembly  
Length=25714846

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features flanking this part of subject sequence:

3698 bp at 5' side: NK2 transcription factor related, locus 5  
79019 bp at 3' side: stanniocalcin 2 precursor

Score = 51.8 bits (56), Expect = 0.004  
Identities = 42/50 (84%), Gaps = 2/50 (4%)  
Strand=Plus/Plus

```
Query 1137      CGGACTCCCAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                |||||
Sbjct 17475370   CGGACTCCCAGC--CTCGGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 17475417
```

Features in this part of subject sequence:  
slit homolog 3

Score = 44.6 bits (48), Expect = 0.62  
Identities = 32/36 (88%), Gaps = 1/36 (2%)  
Strand=Plus/Minus

```
Query 2423      CCTTTTTTCTCCCTCTTTTCC-CCTTGCCCCCTC 2457
                |||||
Sbjct 13112345   CCTTTTTTCTCCCTCTTATCCTCCCTTCCCCCTC 13112310
```

Features flanking this part of subject sequence:

60329 bp at 5' side: HMP19 protein  
556789 bp at 3' side: msh homeobox 2

Score = 42.8 bits (46), Expect = 2.2  
Identities = 32/38 (84%), Gaps = 0/38 (0%)  
Strand=Plus/Plus


```
Query 1999      CTCTGCCCAGCCGGAGGGACGCGGAGGAGGAAGAGGGT 2036
                |||||
Sbjct 18404423   CTCTGCACAGCCGGACAGGTGAGGAGGAGGAAGAGGGT 18404460
```

Features in this part of subject sequence:

SRY (sex determining region Y)-box 30 isoform a  
SRY (sex determining region Y)-box 30 isoform b

Score = 41.0 bits (44), Expect = 7.5  
Identities = 27/30 (90%), Gaps = 0/30 (0%)  
Strand=Plus/Minus

```
Query  528      AAGCGACCCATGAACGCCTTCATGGTGTGG  557
      |||
Sbjct  1885418  AAGCGACCCATGAACGCATTTATGGTTTGG  1885389
```

>ref|NW\_001838022.2|Hs11\_WGA731\_36  Homo sapiens chromosome 11 genomic contig, alternate as  
(based on HuRef SCAF\_1103279188392)  
Length=42354830

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:

SRY (sex determining region Y)-box 6 isoform 1  
SRY (sex determining region Y)-box 6 isoform 2

Score = 50.0 bits (54), Expect = 0.014  
Identities = 65/90 (72%), Gaps = 0/90 (0%)  
Strand=Plus/Plus

```
Query  522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC  581
      |||
Sbjct  34920132  CACATTAAGCGACCAATGAATGCATTTCATGGTTTGGGCAAAGGATGAGAGGAGAAAAATC  34920191

Query  582      ATGGAGCAGTCGCCCCGACATGCACAACGCC  611
      |||
Sbjct  34920192  CTTCAGGCCTTCCCCGACATGCATAACTCC  34920221
```

Features flanking this part of subject sequence:

33 bp at 5' side: mitogen-activated protein kinase 8 interacting protein 1  
13517 bp at 3' side: cryptochrome 2 (photolyase-like)

Score = 41.0 bits (44), Expect = 7.5  
Identities = 35/42 (83%), Gaps = 1/42 (2%)  
Strand=Plus/Minus


```
Query  1155      GCCTCCGCCTCCTTCGGCAGCCTCGGCCTCCGCAGCGCTCGCG  1196
      |||
Sbjct  5001886  GCCTCCGCCTCCTTCGCAGCCGCCCTCCTCCGCGC-CGCG  5001846
```

Features flanking this part of subject sequence:

1290185 bp at 5' side: mucin 15  
199821 bp at 3' side: leucine zipper protein 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus


```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
      |||
Sbjct  25626780  TTGTTGTTGTTGTTGTTGTTGTTGATG  25626754
```

>ref|NW\_001838468.1|Hs18\_WGA1177\_36  Homo sapiens chromosome 18 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188038)  
Length=7515650

Features in this part of subject sequence:  
similar to hCG1790759

Score = 50.0 bits (54), Expect = 0.014  
Identities = 35/40 (87%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGGC*****  2095
      |||
Sbjct  1473112  TTGTTGTTGTTGTTGTTGTTGTTGTTGAAAAAAAAA  1473073
```

>ref|NW\_001838951.1|Hs5\_WGA344\_36  Homo sapiens chromosome 5 genomic contig, alternate asse

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Score = 50.0 bits (54), Expect = 0.014  
Identities = 35/40 (87%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

Features flanking this part of subject sequence:  
 1347233 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing ...  
 881684 bp at 3' side: cytochrome c oxidase subunit VIIc precursor

Score = 44.6 bits (48), Expect = 0.62  
Identities = 33/39 (84%), Gaps = 0/39 (0%)  
Strand=Plus/Plus


Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAAAA	2094
Sbjct	14316178	TTGTTGTTATTGTTGTTCTTATTTATGTTAAAAAAAAA	14316216

```
>ref|NW_001838865.2|Hs2_WGA258_36 Homo sapiens chromosome 2 genomic contig, alternate asse
(based on HuRef SCAF_1103279188138)
Length=7557636
```

Features flanking this part of subject sequence:  
 283252 bp at 5' side: hypothetical protein LOC79843  
 116307 bp at 3' side: plasminogen activator inhibitor type 1, member 2

Score = 50.0 bits (54), Expect = 0.014  
Identities = 35/40 (87%), Gaps = 0/40 (0%)  
Strand=Plus/Plus

Query	2047	GACCTGTGATTGTTGTTATTGATGTTGTTGATGGCAA	2086
Sbjct	1525080	GACCTGGGATTTTGTGTTGTTGTTGTTGTTGTTGGCAA	1525119

>ref|NT\_006576.15|Hs5\_6733  Homo sapiens chromosome 5 genomic contig, reference assembly  
Length=46378398

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Features flanking this part of subject sequence:  
 1500958 bp at 5' side: hypothetical protein  
 319712 bp at 3' side: cadherin 18, type 2 preproprotein

Score = 50.0 bits (54), Expect = 0.014  
Identities = 27/27 (100%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	19126380	TTGTTGTTATTGATGTTGTTGTTGATG	19126354

Features flanking this part of subject sequence:  
2372 bp at 5' side: hypothetical protein  
695213 bp at 3' side: hypothetical protein


Score = 41.0 bits (44), Expect = 7.5  
Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Minus

```
Query 2628      GGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCC 2659
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1877085    GGGGAGCGGGCGGCGGCGGCTGCGGCGACTCC 1877054
```

Features in this part of subject sequence:  
KPL2 protein isoform 1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 2052      GTGATTGTTGTTATTGATGTTGTTGTT 2078
          ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 35740888  GTGGTTGTTGTTATTGTTGTTGTTGTT 35740914
```

>ref|NT\_009237.17|Hs11\_9394  Homo sapiens chromosome 11 genomic contig, reference assembly  
Length=49571094

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
SRY (sex determining region Y)-box 6 isoform 2  
SRY (sex determining region Y)-box 6 isoform 1

Score = 50.0 bits (54), Expect = 0.014  
Identities = 65/90 (72%), Gaps = 0/90 (0%)  
Strand=Plus/Minus

```
Query 522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATC 581
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 14797892  CACATTAAGCGACCAATGAATGCATTTCATGGTTTGGGCAAAGGATGAGAGGAGAAAAATC 14797833

Query 582      ATGGAGCAGTCGCCCCGACATGCACAACGCC 611
          || || || ||||| ||||| ||||| ||||| |||||
Sbjct 14797832  CTTCAGGCCTTCCCCGACATGCATAACTCC 14797803
```

Features flanking this part of subject sequence:  
193583 bp at 5' side: leucine zipper protein 2  
1060010 bp at 3' side: transmembrane protein 16C


Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGTTGATG 2082
          ||||| ||||| ||| ||||| ||||| ||||| |||||
Sbjct 24081028  TTGTTGTTGTTGTTGTTGTTGTTGTTGATG 24081054
```

Features flanking this part of subject sequence:  
13517 bp at 5' side: cryptochrome 2 (photolyase-like)  
33 bp at 3' side: mitogen-activated protein kinase 8 interacting protein 1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 35/42 (83%), Gaps = 1/42 (2%)  
Strand=Plus/Plus

```
Query 1155      GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCGAGCGCTCGCG 1196
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 44694540  GCCTCCGCCTCCTTCGCAGCCGCCGCTCCTCCGCGC-CGCG 44694580
```

>ref|NT\_007819.16|Hs7\_7976  Homo sapiens chromosome 7 genomic contig, reference assembly  
Length=47690382

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features flanking this part of subject sequence:  
627203 bp at 5' side: Sp8 transcription factor isoform 2  
15247 bpat 3' side: Sp4 transcription factor


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71489 bp at 5' side: sodium channel, nonvoltage-gated 1, gamma  
61616 bp at 3' side: sodium channel, nonvoltage-gated 1, beta

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  14611358  TTGTTGTTGTTGATGTTGTTGTTGTTG  14611384
```

>ref|NT\_005403.16|Hs2\_5560  Homo sapiens chromosome 2 genomic contig, reference assembly  
Length=84213157

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features flanking this part of subject sequence:  
127128 bp at 5' side: hypothetical protein  
282932 bp at 3' side: hypothetical protein LOC79843

Score = 50.0 bits (54), Expect = 0.014  
Identities = 35/40 (87%), Gaps = 0/40 (0%)  
Strand=Plus/Minus

```
Query  2047      GACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAA  2086
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  75191620  GACCTGGGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGCAA  75191581
```

Features flanking this part of subject sequence:  
237306 bp at 5' side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga...  
10897 bp at 3' side: potassium inwardly-rectifying channel J3

Score = 42.8 bits (46), Expect = 2.2  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Plus

```
Query  2241      GTTTTGTTTTATTTTGCTTCTTG  2263
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  5753787  GTTTTGTTTTATTTTGCTTCTTG  5753809
```

Features in this part of subject sequence:  
homeobox D11


Score = 42.8 bits (46), Expect = 2.2  
Identities = 28/31 (90%), Gaps = 0/31 (0%)  
Strand=Plus/Minus

```
Query  1159      CCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC  1189
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  27181871  CCGCCTCCTCGGCCGCCGCCGCCGCCGCCGCAGC  27181841
```

Features in this part of subject sequence:  
titin isoform N2-A  
titin isoform novex-1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  29758383  TTGTTGTTGTTGATGTTGTTGTTGTTG  29758357
```

>ref|NT\_006713.14|Hs5\_6870  Homo sapiens chromosome 5 genomic contig, reference assembly  
Length=42230486

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star









Sbjct 26409985 TTGTTGTTGTTGTTGTTGTTGTTGATG 26410011

Features flanking this part of subject sequence:

422057 bp at 5' side: sterile alpha motif domain containing 5  
356529 bp at 3' side: SAM and SH3 domain containing 1

Score = 41.0 bits (44), Expect = 7.5

Identities = 25/27 (92%), Gaps = 0/27 (0%)

Strand=Plus/Plus

Query 2237 CTTGGTTTTGTTTTATTTTGCTTCTTG 2263  
||| |||||  
Sbjct 52412078 CTTTGTGTTGTTTTATTTTGCTTTTTG 52412104

Features in this part of subject sequence:


opioid receptor, mu 1 isoform MOR-10  
phosphoinositide-binding protein PIP3-E

Score = 41.0 bits (44), Expect = 7.5

Identities = 29/32 (90%), Gaps = 1/32 (3%)

Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGCAAA 2087  
||| |||||  
Sbjct 58617258 TTGTTGTTGTTGTTGTTGTTGTTGA-GGCAAA 58617228

>ref|NT\_113898.1|Hs6\_111617  Homo sapiens chromosome 6 genomic contig, reference assembly  
Length=1305230

Features flanking this part of subject sequence:


539 bp at 5' side: similar to HGC6.4  
105 bp at 3' side: similar to myeloid/lymphoid or mixed-lineage leukemia (tr...

Score = 46.4 bits (50), Expect = 0.18

Identities = 31/35 (88%), Gaps = 0/35 (0%)

Strand=Plus/Minus

Query 1155 GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189  
||| |||||  
Sbjct 814424 GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC 814390

>ref|NT\_007302.13|Hs6\_7459  Homo sapiens chromosome 6 genomic contig, reference assembly  
Length=2236975

Features flanking this part of subject sequence:


539 bp at 5' side: hypothetical protein LOC653483  
105 bp at 3' side: myeloid/lymphoid or mixed-lineage leukemia (trithorax hom...

Score = 46.4 bits (50), Expect = 0.18

Identities = 31/35 (88%), Gaps = 0/35 (0%)

Strand=Plus/Minus

Query 1155 GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189  
||| |||||  
Sbjct 185635 GCCTCCGCCTCCGCGGCTGCCTCCGCCTCCGCGGC 185601

>ref|NT\_030059.12|Hs10\_30314  Homo sapiens chromosome 10 genomic contig, reference assembly  
Length=44617998

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features flanking this part of subject sequence:

164871 bp at 5' side: coiled-coil domain containing 147  
21898 bp at 3' side: VPS10 domain receptor protein SORCS 3

Score = 46.4 bits (50), Expect = 0.18

Identities = 28/30 (93%), Gaps = 0/30 (0%)

Strand=Plus/Minus



Features in this part of subject sequence:  
sterolin 1

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||
Sbjct  13885678  TTGTTGTTATTGTTGTTGTTGTTGTTG  13885704
```

Features flanking this part of subject sequence:  
23818 bp at 5' side: M-phase phosphoprotein 10  
14630 bp at 3' side: poly(A) binding protein interacting protein 2B


Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||
Sbjct  41233894  TTGTTGTTATTGTTGTTGTTGTTGCTG  41233868
```

Features flanking this part of subject sequence:  
16873 bp at 5' side: STAM binding protein  
23234 bp at 3' side: actin, gamma 2 propeptide

Score = 41.0 bits (44), Expect = 7.5  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGA  2080
          |||||
Sbjct  43937347  TTGTTGTTATTGTTGTTGTTGTTGA  43937323
```

>ref|NW\_001838115.2|Hs14\_WGA824\_36  Homo sapiens chromosome 14 genomic contig, alternate as  
(based on HuRef SCAF\_1103279188327)  
Length=8970161

Sort alignments for this subject seq  
E value Score Percent identity  
Query start position Subject star

Features in this part of subject sequence:  
REST corepressor 1


Score = 44.6 bits (48), Expect = 0.62  
Identities = 35/42 (83%), Gaps = 0/42 (0%)  
Strand=Plus/Minus

```
Query  1148      CGCCTCGGCCTCCGCTCCTCGGCAGCCTCGGCCTCCGCAGC  1189
          |||||
Sbjct  1645733  CGCCTCGGGCGCCGCCGCTCCTCAGCCTCGGCCGCCGCCGC  1645692
```

Features flanking this part of subject sequence:  
73361 bp at 5' side: SET domain containing 3 isoform b  
65304 bp at 3' side: B-cell CLL/lymphoma 11B isoform 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGA  2080
          |||||
Sbjct  4895427  TTGTTGTTATTGTTGTTGTTGTTGA  4895403
```

>ref|NW\_001838461.1|Hs18\_WGA1170\_36  Homo sapiens chromosome 18 genomic contig, alternate a  
(based on HuRef SCAF\_1103279188344)  
Length=10560353

Features flanking this part of subject sequence:









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462638 bp at 5' side: membrane-associated RING-CH protein I





Query start position Subject star

Features flanking this part of subject sequence:

216269 bp at 5' side: leucine rich repeat containing 8 family, member C  
1792 bp at 3' side: leucine rich repeat containing 8 family, member D

Score = 44.6 bits (48), Expect = 0.62  
Identities = 26/27 (96%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query  2768      GGTTCGGAaaaaaaaaaagaaaaaa 2794
                |||||
Sbjct  60368729  GGTTCGGAAAAAAAAAAAAAAAAAA 60368755
```

Features flanking this part of subject sequence:

30984 bp at 5' side: Cbp/p300-interacting transactivator, with Glu/Asp-rich ca...  
90153 bp at 3' side: CTP synthase

Score = 42.8 bits (46), Expect = 2.2  
Identities = 26/28 (92%), Gaps = 0/28 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGG 2083
                |||||
Sbjct  11330728  TTGTTGTTGTTGTTGTTGTTGTTGATGG 11330701
```

Features flanking this part of subject sequence:

64368 bp at 5' side: discs, large (Drosophila) homolog-associated protein 3  
6709 bp at 3' side: hypothetical protein

Score = 41.0 bits (44), Expect = 7.5  
Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Plus

```
Query  2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082
                |||
Sbjct  5407270  TGTTATTGTTGTTGTTGCTGTTGTTGTTGTTG 5407301
```

Features in this part of subject sequence:

eukaryotic translation initiation factor 2B, subunit 3 gamma

Score = 41.0 bits (44), Expect = 7.5  
Identities = 32/36 (88%), Gaps = 2/36 (5%)  
Strand=Plus/Minus

```
Query  2244      TTGTTTTATTTTG-CTTCTTGGTCAAGAAAGGAGGG 2278
                |||||
Sbjct  15312647  TTGTTTTATTTTGTTTCTTGG-CAAGAGAGGAGGG 15312613
```

Features in this part of subject sequence:

ubiquitin specific protease 24

Score = 41.0 bits (44), Expect = 7.5  
Identities = 28/32 (87%), Gaps = 0/32 (0%)  
Strand=Plus/Minus

```
Query  2056      TTGTTGTTATTGATGTTGTTGTTGATGGCAAA 2087
                |||||
Sbjct  25513245  TTGTTGTTGTTGTTGTTGTTGTTGTTGTCAAA 25513214
```

Features in this part of subject sequence:

DnaJ (Hsp40) homolog, subfamily C, member 6

Score = 41.0 bits (44), Expect = 7.5  
Identities = 36/44 (81%), Gaps = 1/44 (2%)  
Strand=Plus/Plus

```
Query  2049      CCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAA 2092
                |||||
Sbjct  35774590  CCTGTG-TAATTTTGTGTTGTTGTTGTTGTTGGGAAAAAA 35774632
```

Features in this part of subject sequence:

adenylate kinase 5 isoform 1  
adenylate kinase 5 isoform 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query   2053      TGATTGTTGTTATTGATGTTGTTGTTG   2079
          || ||||| ||||| ||||| ||||| |||||
Sbjct   47884298  TGTTTGTTGTTATTGTTGTTGTTGTTG   47884324
```

Features flanking this part of subject sequence:

20976 bp at 5' side: guanylate binding protein 1, interferon-inducible, 67kD  
23939 bp at 3' side: guanylate binding protein 2, interferon-inducible

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus


```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          ||||| ||||| ||||| ||||| ||||| ||
Sbjct   59521838  TTGTTGTTATTGTTGTTGTTGTTGTTG   59521812
```

Features flanking this part of subject sequence:

1219349 bp at 5' side: similar to hCG2040669  
184274 bp at 3' side: polypyrimidine tract binding protein 2

Score = 41.0 bits (44), Expect = 7.5  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          ||||| ||||| ||||| ||||| ||||| ||
Sbjct   66975040  TTGTTGTTATTGTTGTTGTTGTTGTTG   66975066
```

>ref|NT\_010859.14|Hs18\_11016  Homo sapiens chromosome 18 genomic contig, reference assembly  
Length=15400898

Features flanking this part of subject sequence:

37804 bp at 5' side: hypothetical protein  
48190 bp at 3' side: erythrocyte membrane protein band 4.1-like 3

Score = 44.6 bits (48), Expect = 0.62  
Identities = 29/32 (90%), Gaps = 0/32 (0%)  
Strand=Plus/Minus

```
Query   2050      CTGTGATTGTTGTTATTGATGTTGTTGTTGAT   2081
          |||| | ||||| ||||| ||||| ||||| |||||
Sbjct   5336492  CTGTTGTTGTTGTTATTGTTGTTGTTGTTGAT   5336461
```

Database: human build 36.3 reference assembly genomic scaffolds

Posted date: Apr 16, 2008 7:40 PM

Number of letters in database: 1,523,044,440

Number of sequences in database: 49,942

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.634	0.408	0.912

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 49942

Number of Hits to DB: 5820376

Number of extensions: 423311

Number of successful extensions: 1102



Number of sequences better than 10: 52  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 1085  
Number of HSP's successfully gapped: 58  
Length of query: 2797  
Length of database: 5818011736  
Length adjustment: 35  
Effective length of query: 2762  
Effective length of database: 5816263766  
Effective search space: 16064520521692  
Effective search space used: 16064520521692  
A: 0  
X1: 22 (20.1 bits)  
X2: 33 (29.8 bits)  
X3: 110 (99.2 bits)  
S1: 36 (33.7 bits)  
S2: 44 (41.0 bits)



